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(54) Title: NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH AND DEVELOPMENT AND USES THEREOF

(57) Abstract: Nucleotide sequences are isolated from Arabidopsis thaliana that code for proteins essential for plant growth and development. The essentially of the proteins may be exploited by recombinantly expressing the proteins and using them in screening assays to identify compounds that interact with or inhibit the proteins and are therefore potential herbicides.

NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH AND DEVELOPMENT AND USES THEREOF

The present invention pertains to nucleic acid molecules isolated from *Arabidopsis*

5 *thaliana* comprising nucleotide sequences that encode proteins essential for plant growth and development. The invention particularly relates to methods of using these proteins as herbicide targets, based on this essentiality.

The use of herbicides to control undesirable vegetation such as weeds in crop fields

10 has become almost a universal practice. The herbicide market exceeds 15 billion dollars annually. Despite this extensive use, weed control remains a significant and costly problem for farmers.

Effective use of herbicides requires sound management. For instance, the time and method of application and stage of weed plant development are critical to achieving good

15 weed control with herbicides. Because various weed species are resistant to herbicides, the production of effective new herbicides becomes increasingly important. New herbicides can now be discovered using high-throughput screens that implement recombinant DNA technology. Metabolic enzymes found to be essential to plant growth and development can be recombinantly produced through standard molecular biological techniques and utilized as

20 herbicide targets in screens for novel inhibitors of the enzyme activity. More generally, any essential plant protein can be used to screen for inhibitors of its activity. The novel inhibitors discovered through such screens may then be used as herbicides to control undesirable vegetation.

In view of the above, there remain persistent and ongoing problems with unwanted or

25 detrimental vegetation growth (*e.g.* weeds). Furthermore, as the population continues to grow, there will be increasing food shortages. Therefore, there exists a long felt, yet unfulfilled need, to find new, effective, and economic herbicides.

In view of these needs, it is an object of the invention to provide nucleic acid

30 molecules from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant growth and development. It is another object to provide the essential proteins encoded by these essential nucleotide sequences for assay development to identify

inhibitory compounds with herbicidal activity. It is still another object of the present invention to provide an effective and beneficial method for identifying new or improved herbicides using the essential proteins of the invention.

In furtherance of these and other objects, the present invention provides nucleic acid molecules isolated from *Arabidopsis thaliana* comprising nucleotide sequences that encode proteins essential for plant viability. Genetic results show that when any of the nucleotide sequences of the invention are mutated in *Arabidopsis thaliana*, the resulting phenotype is embryo or seedling lethal in the homozygous state. In particular, by using *Ac/Ds* transposon or T-DNA-mediated mutagenesis, the inventors of the present invention are the first to demonstrate that the activity of each protein of the present invention is essential for plant growth in *Arabidopsis thaliana*.

This knowledge is exploited to provide novel herbicide modes of action. The critical role in plant growth of the proteins encoded by each of the nucleotide sequences of the invention implies that chemicals that inhibit the function of any one of these proteins in plants are likely to have detrimental effects on plants and are potentially good herbicide candidates. Thus, the proteins encoded by the essential nucleotide sequences provide the bases for assays designed to easily and rapidly identify novel herbicides.

The present invention therefore provides methods of using a purified protein encoded by any one of the nucleotide sequences described below to identify inhibitors thereof, which can then be used as herbicides to suppress the growth of undesirable vegetation, *e.g.* in fields where crops are grown, particularly agronomically important crops such as maize and other cereal crops such as wheat, oats, rye, sorghum, rice, barley, millet, turf and forage grasses, and the like, as well as cotton, sugar cane, sugar beet, oilseed rape, and soybeans.

Disclosed herein are nucleic acid molecules isolated from *Arabidopsis thaliana*. In one embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence, the complement of which hybridizes under stringent conditions to a sequence selected from the group consisting of the odd numbered SEQ ID NOs:1-95. In another embodiment, the present invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a protein comprising an amino acid sequence having at least 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

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The present invention also provides a chimeric construct comprising a promoter operatively linked to a nucleic acid molecule according to the present invention, wherein the promoter is preferably functional in a eukaryote, wherein the promoter is preferably heterologous to the nucleic acid molecule. The present invention further provides a

5   recombinant vector comprising a chimeric construct according to the present invention, wherein said vector is capable of being stably transformed into a host cell. The present invention still further provides a host cell comprising a nucleic acid molecule according to the present invention, wherein said nucleic acid molecule is preferably expressible in the cell. The host cell is preferably selected from the group consisting of a plant cell, a yeast cell, an

10   insect cell, and a prokaryotic cell. The present invention additionally provides a plant or seed comprising a plant cell according to the present invention.

The present invention also provides proteins essential for plant growth in *Arabidopsis thaliana*. In one embodiment, the present invention provides an isolated protein comprising an amino acid sequence having at least 60%, preferably 70%, more preferably 80%, still more

15   preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. In accordance with another embodiment, the present invention also relates to the recombinant production of proteins of the invention and methods of using the proteins of the invention in assays for identifying compounds that interact with the protein.

20   According to another aspect, the present invention provides a method of identifying a herbicidal compound, comprising: (a) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to bind to said polypeptide, under conditions conducive to binding; (b) selecting a compound

25   identified in (a) that binds to said polypeptide; (c) applying a compound selected in (b) to a plant to test for herbicidal activity; and (d) selecting a compound identified in (c) that has herbicidal activity. Preferably, the polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. More preferably, the polypeptide comprises an amino acid

30   sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. Most preferably, the polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID

NOs:2-96. The present invention also provides a method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to this method.

According to yet another aspect, the present invention provides a method of

5   identifying a herbicidal compound, comprising: (a) combining a polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to inhibit the activity of said polypeptide, under conditions conducive to inhibition; (b) selecting a compound identified in (a) that inhibits the activity of said polypeptide; (c)

10   applying a compound selected in (b) to a plant to test for herbicidal activity; and (d) selecting a compound identified in (c) that has herbicidal activity. Preferably, the polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. More preferably, the polypeptide comprises an amino acid sequence at least 99% identical to an amino acid

15   sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. Most preferably, the polypeptide comprises an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96. The present invention also provides a method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to this method.

20   The present invention still further provides a method for killing or inhibiting the growth or viability of a plant, comprising inhibiting expression in said plant of a protein having at least 60%, preferably 70%, more preferably 80%, still more preferably 90%, even more preferably 95%, and most preferably 99-100% sequence identity to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

25   Other objects and advantages of the present invention will become apparent to those skilled in the art and from a study of the following description of the invention and non-limiting examples. The entire contents of all publications mentioned herein are hereby incorporated by reference.

30   BRIEF DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

Odd numbered SEQ ID NOs:1-95 are nucleotide sequences isolated from *Arabidopsis thaliana* that are more fully described in Table 5 below.

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Even numbered SEQ ID NOs:2-96 are protein sequences encoded by the immediately preceding nucleotide sequence, *e.g.*, SEQ ID NO:2 is the protein encoded by the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:4 is the protein encoded by the nucleotide sequence of SEQ ID NO:3, etc.

5   SEQ ID NOs:101-125 are PCR primers.

DEFINITIONS

For clarity, certain terms used in the specification are defined and presented as follows:

10   "Associated with / operatively linked" refer to two nucleic acid sequences that are related physically or functionally. For example, a promoter or regulatory DNA sequence is said to be "associated with" a DNA sequence that codes for an RNA or a protein if the two sequences are operatively linked, or situated such that the regulator DNA sequence will affect the expression level of the coding or structural DNA sequence.

15   A "chimeric construct" is a recombinant nucleic acid sequence in which a promoter or regulatory nucleic acid sequence is operatively linked to, or associated with, a nucleic acid sequence that codes for an mRNA or which is expressed as a protein, such that the regulatory nucleic acid sequence is able to regulate transcription or expression of the associated nucleic acid sequence. The regulatory nucleic acid sequence of the chimeric construct is not normally

20   operatively linked to the associated nucleic acid sequence as found in nature.

Co-factor: natural reactant, such as an organic molecule or a metal ion, required in an enzyme-catalyzed reaction. A co-factor is *e.g.* NAD(P), riboflavin (including FAD and FMN), folate, molybdopterin, thiamin, biotin, lipoic acid, pantothenic acid and coenzyme A, S-adenosylmethionine, pyridoxal phosphate, ubiquinone, menaquinone. Optionally, a co-factor

25   can be regenerated and reused.

A "coding sequence" is a nucleic acid sequence that is transcribed into RNA such as mRNA, rRNA, tRNA, snRNA, sense RNA or antisense RNA. Preferably the RNA is then translated in an organism to produce a protein.

Complementary: "complementary" refers to two nucleotide sequences that comprise

30   antiparallel nucleotide sequences capable of pairing with one another upon formation of hydrogen bonds between the complementary base residues in the antiparallel nucleotide sequences.

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Enzyme activity: means herein the ability of an enzyme to catalyze the conversion of a substrate into a product. A substrate for the enzyme comprises the natural substrate of the enzyme but also comprises analogues of the natural substrate, which can also be converted, by the enzyme into a product or into an analogue of a product. The activity of the enzyme is

5   measured for example by determining the amount of product in the reaction after a certain period of time, or by determining the amount of substrate remaining in the reaction mixture after a certain period of time. The activity of the enzyme is also measured by determining the amount of an unused co-factor of the reaction remaining in the reaction mixture after a certain period of time or by determining the amount of used co-factor in the reaction mixture after a

10   certain period of time. The activity of the enzyme is also measured by determining the amount of a donor of free energy or energy-rich molecule (e.g. ATP, phosphoenolpyruvate, acetyl phosphate or phosphocreatine) remaining in the reaction mixture after a certain period of time or by determining the amount of a used donor of free energy or energy-rich molecule (e.g. ADP, pyruvate, acetate or creatine) in the reaction mixture after a certain period of time.

15   Essential: an "essential" *Arabidopsis thaliana* nucleotide sequence is a nucleotide sequence encoding a protein such as *e.g.* a biosynthetic enzyme, receptor, signal transduction protein, structural gene product, or transport protein that is essential to the growth or survival of the plant.

Expression Cassette: "Expression cassette" as used herein means a nucleic acid

20   molecule capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operatively linked to the nucleotide sequence of interest which is operatively linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example

25   antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one that is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression

30   cassette is heterologous with respect to the host, *i.e.*, the particular DNA sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of

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the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter that initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, such as a plant, the promoter can also be specific to a particular tissue or organ or stage of

5   development.

Gene: the term "gene" is used broadly to refer to any segment of DNA associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety

10   of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

Heterologous/exogenous: The terms "heterologous" and "exogenous" when used herein to refer to a nucleic acid sequence (*e.g.* a DNA sequence) or a gene, refer to a sequence

15   that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or

20   heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" nucleic acid (*e.g.* DNA) sequence is a nucleic acid (*e.g.* DNA) sequence naturally associated with a host cell into which it is introduced.

25   Hybridization: The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be

30   accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

Inhibitor: a chemical substance that inactivates the enzymatic activity of a protein such as a biosynthetic enzyme, receptor, signal transduction protein, structural gene product, or transport protein. The term "herbicide" (or "herbicidal compound") is used herein to define an inhibitor applied to a plant at any stage of development, whereby the herbicide inhibits the

5   growth of the plant or kills the plant.

Interaction: quality or state of mutual action such that the effectiveness or toxicity of one protein or compound on another protein is inhibitory (antagonists) or enhancing (agonists).

A nucleic acid sequence is "isocoding with" a reference nucleic acid sequence when

10   the nucleic acid sequence encodes a polypeptide having the same amino acid sequence as the polypeptide encoded by the reference nucleic acid sequence.

Isogenic: plants that are genetically identical, except that they may differ by the presence or absence of a heterologous DNA sequence.

Isolated: in the context of the present invention, an isolated DNA molecule or an

15   isolated enzyme is a DNA molecule or enzyme that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or enzyme may exist in a purified form or may exist in a non-native environment such as, for example, in a transgenic host cell.

Mature protein: protein from which the transit peptide, signal peptide, and/or

20   propeptide portions have been removed.

Minimal Promoter: the smallest piece of a promoter, such as a TATA element, that can support any transcription. A minimal promoter typically has greatly reduced promoter activity in the absence of upstream activation. In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription.

25   Modified Enzyme Activity: enzyme activity different from that which naturally occurs in a plant (*i.e.* enzyme activity that occurs naturally in the absence of direct or indirect manipulation of such activity by man), which is tolerant to inhibitors that inhibit the naturally occurring enzyme activity.

Native: refers to a gene that is present in the genome of an untransformed plant cell.

30   Naturally occurring: the term "naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism (including a virus), which can be

isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

Nucleic acid: the term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. Unless specifically limited,

5   the term encompasses nucleic acids containing known analogues of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof *(e.g.* degenerate codon substitutions) and complementary sequences and as well as the sequence

10 explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al., Nucleic Acid Res.* 19: · 5081 (1991); Ohtsuka *et al., J. Biol. Chem.* 260: 2605-2608 (1985); Rossolini *et al., Mol. Cell. Probes* 8: 91-98 (1994)). The terms "nucleic acid" or "nucleic acid sequence" may also

15 be used interchangeably with gene, cDNA, and mRNA encoded by a gene.

"ORF" means open reading frame.

Percent identity: the phrases "percent identical" or "percent identical," in the context of two nucleic acid or protein sequences, refers to two or more sequences or subsequences that have for example 60%, preferably 70%, more preferably 80%, still more preferably 90%,

20 even more preferably 95%, and most preferably at least 99% nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection. Preferably, the percent identity exists over a region of the sequences that is at least about 50 residues in length, more preferably over a region of at least about 100 residues, and most preferably the

25 percent identity exists over at least about 150 residues. In an especially preferred embodiment, the percent identity exists over the entire length of the coding regions.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if

30 necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

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Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2: 482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48: 443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85: 2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (*see generally,* Ausubel *et al., infra*).

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al., J. Mol. Biol.* 215: 403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, $M=5$, $N=-4$, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89: 10915 (1989)).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.*, Karlin &

Altschul, *Proc. Nat'l. Acad. Sci. USA* 90: 5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered

5   similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

Pre-protein: protein that is normally targeted to a cellular organelle, such as a chloroplast, and still comprises its native transit peptide.

10   Purified: the term "purified," when applied to a nucleic acid or protein, denotes that the nucleic acid or protein is essentially free of other cellular components with which it is associated in the natural state. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high

15   performance liquid chromatography. A protein that is the predominant species present in a preparation is substantially purified. The term "purified" denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the nucleic acid or protein is at least about 50% pure, more preferably at least about 85% pure, and most preferably at least about 99% pure.

20   Two nucleic acids are "recombined" when sequences from each of the two nucleic acids are combined in a progeny nucleic acid. Two sequences are "directly" recombined when both of the nucleic acids are substrates for recombination. Two sequences are "indirectly recombined" when the sequences are recombined using an intermediate such as a cross-over oligonucleotide. For indirect recombination, no more than one of the sequences is an actual

25   substrate for recombination, and in some cases, neither sequence is a substrate for recombination.

"Regulatory elements" refer to sequences involved in controlling the expression of a nucleotide sequence. Regulatory elements comprise a promoter operatively linked to the nucleotide sequence of interest and termination signals. They also typically encompass

30   sequences required for proper translation of the nucleotide sequence.

Significant Increase: an increase in enzymatic activity that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater

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of the activity of the wild-type enzyme in the presence of the inhibitor, more preferably an increase by about 5-fold or greater, and most preferably an increase by about 10-fold or greater.

Significantly less: means that the amount of a product of an enzymatic reaction is
5   reduced by more than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater of the activity of the wild-type enzyme in the absence of the inhibitor, more preferably an decrease by about 5-fold or greater, and most preferably an decrease by about 10-fold or greater.

Specific Binding/Immunological Cross-Reactivity: An indication that two nucleic
10   acid sequences or proteins are substantially identical is that the protein encoded by the first nucleic acid is immunologically cross reactive with, or specifically binds to, the protein encoded by the second nucleic acid. Thus, a protein is typically substantially identical to a second protein, for example, where the two proteins differ only by conservative substitutions. The phrase "specifically (or selectively) binds to an antibody," or "specifically (or selectively)
15   immunoreactive with," when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions
20   may require an antibody that is selected for its specificity for a particular protein. For example, antibodies raised to the protein with the amino acid sequence encoded by any of the nucleic acid sequences of the invention can be selected to obtain antibodies specifically immunoreactive with that protein and not with other proteins except for polymorphic variants. A variety of immunoassay formats may be used to select antibodies specifically
25   immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays, Western blots, or immunohistochemistry are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, A Laboratory Manual,* Cold Spring Harbor Publications, New York "Harlow and Lane"), for a description of immunoassay formats and conditions that can be used to determine specific
30   immunoreactivity. Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

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"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. An extensive

5 guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic* Acid Probes part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at

10 a defined ionic strength and pH. Typically, under "stringent conditions" a probe will hybridize to its target subsequence, but to no other sequences.

The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent hybridization

15 conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is 50% formamide with 1 mg of heparin at 42°C, with the hybridization being carried out overnight. An example of highly stringent wash conditions is 0.1 5M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2x SSC wash at 65°C for 15 minutes (*see,* Sambrook, *infra,*

20 for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, *e.g.,* more than 100 nucleotides, is 1x SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, *e.g.,* more than 100 nucleotides, is 4-6x SSC at 40°C for 15 minutes. For short probes (*e.g.,* about 10 to 50 nucleotides), stringent conditions

25 typically involve salt concentrations of less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a

30 specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially

identical. This occurs, *e.g.*, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

The following are examples of sets of hybridization/wash conditions that may be used to clone nucleotide sequences that are homologues of reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

A "subsequence" refers to a sequence of nucleic acids or amino acids that comprise a part of a longer sequence of nucleic acids or amino acids (*e.g.*, protein) respectively.

Substrate: a substrate is the molecule that an enzyme naturally recognizes and converts to a product in the biochemical pathway in which the enzyme naturally carries out its function, or is a modified version of the molecule, which is also recognized by the enzyme and is converted by the enzyme to a product in an enzymatic reaction similar to the naturally-occurring reaction.

Transformation: a process for introducing heterologous DNA into a plant cell, plant tissue, or plant. Transformed plant cells, plant tissue, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof.

"Transformed," "transgenic," and "recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof. A "non-transformed," "non-transgenic," or "non-recombinant" host refers to a wild-type organism, *e.g.*, a bacterium or plant, which does not contain the heterologous nucleic acid molecule.

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Viability: "viability" as used herein refers to a fitness parameter of a plant. Plants are assayed for their homozygous performance of plant development, indicating which proteins are essential for plant growth.

5   I.   Identification of Essential *Arabidopsis thaliana* Nucleotide Sequences and Encoded Proteins Using *Ac/Ds* Transposon or T-DNA-Mediated Mutagenesis

As shown in the examples below, the essentiality of the nucleotide sequences described herein for normal plant growth and development, have been demonstrated for the first time in *Arabidopsis* using *Ac/Ds* transposon or T-DNA-mediated mutagenesis. Having

10   established the essentiality of the function of the encoded proteins in *Arabidopsis thaliana* and having identified the nucleotide sequences encoding these essential proteins, the inventors thereby provide an important and sought after tool for new herbicide development.

Arabidopsis insertional mutant lines segregating for seedling lethal mutations are identified as a first step in the identification of essential proteins. Starting with T2 seeds

15   collected from single T1 plants containing T-DNA insertions in their genomes, those lines segregating homozygous seedling lethal seedlings are identified. Ds transposon insertion lines are produced as described in Sundaresan *et al.* (1995) (Genes and Dev., 9:1797-1810), incorporated herein by reference. Starting with F3 or F4 seeds collected from single F2 or F3 kanamycin-resistant plants containing *Ds* insertions in their genomes (see Figure 3 of

20   Sundaresan *et al.* (1995) (Genes and Dev., 9:1797-1810), those lines segregating homozygous seedling lethal seedlings are identified. These lines are found by placing seeds onto minimal plant growth media, which contains the fungicides benomyl and maxim, and screening for inviable seedlings after 7 and 14 days in the light at room temperature. Inviable phenotypes include altered pigmentation or altered morphology. These phenotypes are observed either on

25   plates directly or in soil following transplantation of seedlings.

Essential genes are also identified through the isolation of lethal mutants blocked in early development. Examples of lethal mutants include those blocked in the formation of the male or female gametes or embryo. Gametophytic mutants are found by examining T1 insertion lines for the presence of 50% aborted pollen grains or ovules. Embryo defective

30   mutants produce 25% defective seeds following self-pollination of T1 plants (see Errampalli *et al.* 1991, Plant Cell 3:149-157; Castle *et al.* 1993, Mol Gen Genet 241:504-514).

When a line is identified as segregating a seedling lethal or an embryo defective phenotype, it is determined if the resistance marker in the *Ds* transposon or T-DNA insertion co-segregates with the lethality (Errampalli *et al.* (1991) The Plant Cell, 3:149-157). Cosegregation analysis is done by placing the seeds on media containing the selective agent

5   and scoring the seedlings for resistance or sensitivity to the agent. Examples of selective agents used are kanamycin, hygromycin, or phosphinothricin. About 35 resistant seedlings are transplanted to soil and their progeny are examined for the segregation of the seedling lethal. In the case in which the *Ds* transposon or T-DNA insertion disrupts an essential gene, there is co-segregation of the resistance phenotype and the seedling lethal or embryo defective

10 phenotype in every plant. Therefore, in such a case, all resistant plants segregate a seedling lethal or embryo defective phenotype in the next generation; this result indicates that each of the resistant plants is heterozygous for the mutation and hemizygous for the T-DNA insert causing the mutation.

For the *Arabidopsis* lines showing co-segregation of the transposon-encoded or T-

15 DNA-encoded resistance marker and the lethal phenotype, PCR-based molecular approaches such as, TAIL-PCR (Liu *et al.* (1995) Plant J., 8:457-463; Liu and Whittier (1995), Genomics, 25:674-681), TAIL2k, vectorette PCR (Riley *et al.* (1990) Nucleic Acids Research, 18: 2887-2890)), or the GenomeWalker™ kit (CLONTECH Laboratories, Inc., Palo Alto, CA), may be used to directly amplify the plant DNA fragments flanking the transposon or T-DNA. Each

20 of these techniques utilizes the known sequence of the transposon or T-DNA, and can be used to recover small (less than 5 kb) fragments directly adjacent to the insertion. PCR products are isolated and their DNA sequence is determined.

Alternatively, plasmid rescue may be used to isolate the plant DNA/T-DNA border fragments. Southern blot analysis may be performed as an initial step in the characterization

25 of the molecular nature of each insertion. Southern blots are done with genomic DNA isolated from heterozygotes and using probes capable of hybridizing with the T-DNA vector DNA. Using the results of the Southern analysis, appropriate restriction enzymes are chosen to perform plasmid rescue in order to molecularly clone *Arabidopsis thaliana* genomic DNA flanking one or both sides of the T-DNA insertion. Plasmids obtained in this manner are

30 analyzed by restriction enzyme digestion to sort the plasmids into classes based on their digestion pattern. For each class of plasmid clone, the DNA sequence is determined.

· The resulting sequences, obtained by any of the above outlined approaches, are analyzed for the presence of non-*Ds* transposon and non-T-DNA vector sequences, as appropriate. When such sequences are found, they are used to search DNA and protein databases using the BLAST and BLAST2 programs (Altschul *et al.* (1990) *J Mol. Biol.* 215:

5   403-410; Altschul *et al.* (1997) *Nucleic Acid Res.* 25:3389-3402, both incorporated herein by reference). Additional genomic and cDNA sequences for each gene are identified by standard molecular biology procedures.

II.   Recombinant Production Of Essential Proteins And Uses Thereof

10   For recombinant production of a protein of the invention in a host organism, a nucleotide sequence encoding the protein is inserted into an expression cassette designed for the chosen host and introduced into the host where it is recombinantly produced. The choice of the specific regulatory sequences such as promoter, signal sequence, 5' and 3' untranslated sequence, and enhancer appropriate for the chosen host is within the level of the skill of the

15   routineer in the art. The resultant molecule, containing the individual elements linking in the proper reading frame, is inserted into a vector capable of being transformed into the host cell. Suitable expression vectors and methods for recombinant production of proteins are well known for host organisms such as *E. coli*, yeast, and insect cells (see, *e.g.*, Lucknow and Summers, *Bio/Technol.* 6:47 (1988)). Additional suitable expression vectors are baculovirus

20   expression vectors, *e.g.*, those derived from the genome of *Autographica californica* nuclear polyhedrosis virus (AcMNPV). A preferred baculovirus/insect system is PVL1392(3) used to transfect *Spodoptera frugiperda* SF9 cells (ATCC) in the presence of linear *Autographica californica* baculovirus DNA (Phramingen, San Diego, CA). The resulting virus is used to infect HighFive *Tricoplusia ni* cells (Invitrogen, La Jolla, CA).

25   Recombinantly produced proteins are isolated and purified using a variety of standard techniques. The actual techniques used vary depending upon the host organism used, whether the protein is designed for secretion, and other such factors. Such techniques are well known to the skilled artisan (*see, e.g.* chapter 16 of Ausubel, F. *et al.*, "Current Protocols in Molecular Biology", pub. by John Wiley & Sons, Inc. (1994).

30

III.   Assays For Characterizing The Essential Proteins

The recombinantly produced proteins described herein are useful for a variety of purposes. For example, they can be used in *in vitro* assays to screen known herbicidal chemicals whose target has not been identified to determine if they inhibit protein activity.

5.   Such *in vitro* assays may also be used as more general screens to identify chemicals that inhibit such protein activity and that are therefore novel herbicide candidates. Recombinantly produced proteins may also be used to elucidate the complex structure of these molecules and to further characterize their association with known inhibitors in order to rationally design new inhibitory herbicides. Alternatively, the recombinant protein can be used to isolate

10   antibodies or peptides that modulate the activity and are useful in transgenic solutions.

IV.   *In vitro* Inhibitor Assay: Discovery of Small Molecule Ligands That Interact with Essential Proteins Of Unknown Biochemical Function

Once a protein has been identified as a potential herbicide target based on its

15   essentiality for normal plant growth and viability, a next step is to develop an assay that allows screening large number of chemicals to determine which ones interact with the protein. Although it is straightforward to develop assays for proteins of known function, developing assays with proteins of unknown functions can be more difficult.

To address this issue, novel technologies are used that can detect interactions between

20   a protein and a compound without knowing the biological function of the protein. A short description of three methods is presented, including fluorescence correlation spectroscopy, surface-enhanced laser desorption/ionization, and biacore technologies.

Fluorescence Correlation Spectroscopy (FCS) theory was developed in 1972 but it is only in recent years that the technology to perform FCS became available (Madge *et al.*

25   (1972) Phys. Rev. Lett., 29: 705-708; Maiti *et al.* (1997) Proc. Natl. Acad. Sci. USA, 94: 11753-11757). FCS measures the average diffusion rate of a fluorescent molecule within a small sample volume. The sample size can be as low as 10^3 fluorescent molecules and the sample volume as low as the cytoplasm of a single bacterium. The diffusion rate is a function of the mass of the molecule and decreases as the mass increases. FCS can therefore be

30   applied to protein-ligand interaction analysis by measuring the change in mass and therefore in diffusion rate of a molecule upon binding. In a typical experiment, the target to be analyzed is expressed as a recombinant protein with a sequence tag, such as a poly-histidine

sequence, inserted at the N or C-terminus. The expression takes place in _E. coli_, yeast or insect cells. The protein is purified by chromatography. For example, the poly-histidine tag can be used to bind the expressed protein to a metal chelate column such as Ni2+ chelated on iminodiacetic acid agarose. The protein is then labeled with a fluorescent tag such as

5   carboxytetramethylrhodamine or BODIPY® (Molecular Probes, Eugene, OR). The protein is then exposed in solution to the potential ligand, and its diffusion rate is determined by FCS using instrumentation available from Carl Zeiss, Inc. (Thornwood, NY). Ligand binding is determined by changes in the diffusion rate of the protein.

Surface-Enhanced Laser Desorption/Ionization (SELDI) was invented by Hutchens

10   and Yip during the late 1980's (Hutchens and Yip (1993) Rapid Commun. Mass Spectrom. 7: 576-580). When coupled to a time-of-flight mass spectrometer (TOF), SELDI provides a mean to rapidly analyze molecules retained on a chip. It can be applied to ligand-protein interaction analysis by covalently binding the target protein on the chip and analyze by MS the small molecules that bind to this protein (Worrall _et al._ (1998) Anal. Biochem. 70: 750-

15   756). In a typical experiment, the target to be analyzed is expressed as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the SELDI chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via, for example, a delivery system capable to pipette the ligands in a sequential

20   manner (autosampler). The chip is then submitted to washes of increasing stringency, for example a series of washes with buffer solutions containing an increasing ionic strength. After each wash, the bound material is analyzed by submitting the chip to SELDI-TOF. Ligands that specifically bind the target will be identified by the stringency of the wash needed to elute them.

25   Biacore relies on changes in the refractive index at the surface layer upon binding of a ligand to a protein immobilized on the layer. In this system, a collection of small ligands is injected sequentially in a 2-5 microlitre cell with the immobilized protein. Binding is detected by surface plasmon resonance (SPR) by recording laser light refracting from the surface. In general, the refractive index change for a given change of mass concentration at the surface

30   layer, is practically the same for all proteins and peptides, allowing a single method to be applicable for any protein (Liedberg _et al._ (1983) Sensors Actuators 4: 299-304; Malmquist (1993) Nature, 361: 186-187). In a typical experiment, the target to be analyzed is expressed

as described for FCS. The purified protein is then used in the assay without further preparation. It is bound to the Biacore chip either by utilizing the poly-histidine tag or by other interaction such as ion exchange or hydrophobic interaction. The chip thus prepared is then exposed to the potential ligand via the delivery system incorporated in the instruments

5   sold by Biacore (Uppsala, Sweden) to pipette the ligands in a sequential manner (autosampler). The SPR signal on the chip is recorded and changes in the refractive index indicate an interaction between the immobilized target and the ligand. Analysis of the signal kinetics on rate and off rate allows the discrimination between non-specific and specific interaction.

10   Another assay for small molecule ligands that interact with a polypeptide is an inhibitor assay. For example, such an inhibitor assay useful for identifying inhibitors of the products of essential plant nucleic acid sequences, such as the essential *Arabidopsis* proteins described herein, comprises the steps of:

a) reacting an essential *Arabidopsis* protein described herein and a substrate thereof in

15   the presence of a suspected inhibitor of the protein's function;

b) comparing the rate of enzymatic activity of the protein in the presence of the suspected inhibitor to the rate of enzymatic activity under the same conditions in the absence of the suspected inhibitor; and

c) determining whether the suspected inhibitor inhibits the essential *Arabidopsis*

20   protein.

For example, the inhibitory effect on the activity of a hereindescribed essential *Arabidopsis* protein, may be determined by a reduction or complete inhibition of protein activity in the assay. Such a determination may be made by comparing, in the presence and absence of the candidate inhibitor, the amount of substrate used or intermediate or product

25   made during the reaction.

V.   Production of peptides

Phage particles displaying diverse peptide libraries permits rapid library construction, affinity selection, amplification and selection of ligands directed against an essential protein

30   (H.B. Lowman, *Annu. Rev. Biophys. Biomol. Struct.* 26, 401-424 (1997)). Structural analysis of these selectants can provide new information about ligand-target molecule interactions and

then in the process also provide a novel molecule that can enable the development of new

herbicides based upon these peptides as leads.

VI.   *In Vivo* Inhibitor Assay

5   In one embodiment, a suspected herbicide, for example identified by *in vitro*

screening, is applied to plants at various concentrations. The suspected herbicide is preferably

sprayed on the plants. After application of the suspected herbicide, its effect on the plants, for

example death or suppression of growth is recorded.

In another embodiment, an *in vivo* screening assay for inhibitors of the activity of a

10   hereindescribed essential protein uses transgenic plants, plant tissue, plant seeds or plant cells

capable of overexpressing a nucleotide sequence disclosed herein that encodes an essential

protein, wherein the essential protein is enzymatically active in the transgenic plants, plant

tissue, plant seeds or plant cells. A chemical is then applied to the transgenic plants, plant

tissue, plant seeds or plant cells and to the isogenic non-transgenic plants, plant tissue, plant

15   seeds or plant cells, and the growth or viability of the transgenic and non-transformed plants,

plant tissue, plant seeds or plant cells are determined after application of the chemical and

compared. Compounds capable of inhibiting the growth of the non-transgenic plants, but not

affecting the growth of the transgenic plants are selected as specific inhibitors of the essential

protein's activity.

20   The invention will be further described by reference to the following detailed

examples. These examples are provided for purposes of illustration only, and are not intended

to be limiting unless otherwise specified.

EXAMPLES

25   Standard recombinant DNA and molecular cloning techniques used here are well

known in the art and are described by J. Sambrook, *et al.*, Molecular Cloning: A *Laboratory*

Manual, 3d Ed., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (2001); by

T.J. Silhavy, M.L. Berman, and L.W. Enquist, *Experiments with Gene Fusions*, Cold Spring

Harbor Laboratory, Cold Spring Harbor, NY (1984) and by Ausubel, F.M. *et al., Current*

30   *Protocols in Molecular Biology*, New York, John Wiley and Sons Inc., (1988), Reiter, *et al.,*

Methods in Arabidopsis Research, World Scientific Press (1992), and Schultz *et al., Plant*

Molecular Biology Manual, Kluwer Academic Publishers (1998). These references describe

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the standard techniques used for all steps in tagging and cloning genes from *Ac/Ds* transposon or T-DNA mutagenized populations of *Arabidopsis*: plant infection and transformation; screening for the identification of seedling mutants; and cosegregation analysis. *Ds* transposon insertion lines produced as described in Sundaresan *et al.* (1995) Genes and Dev.,

5   9:1797-1810) are used in these experiments. T-DNA lines are generated using vacuum infiltration or floral dip methods (Bechtold *et al.* (1993) C. R. Acad. Sci. Paris, 316:1194-1199; Clough and Bent (1998) Plant J., 16:735-743; Desfeux *et al.* (2000) Plant Physiol., 123:895-904).

10   Example 1:   Identification of *Arabidopsis* Mutants with Lethal Phenotypes
            Essential genes are identified through the isolation of lethal mutants blocked in early development. Examples of lethal mutants include those blocked in the formation of the male or female gametes, embryo, or resulting seedling. Gametophytic mutants are found by examining insertion lines for the presence of 50% aborted pollen grains or ovules. Embryo

15   defective lethal mutants usually produce 25% defective seeds following self-pollination of plants heterozygous for an insertion (see Errampalli *et al.* 1991, Plant Cell 3:149-157; Castle *et al.* 1993, Mol Gen Genet 241:504-514). Seedling lethal mutants usually segregate 25% seedlings that exhibit a lethal phenotype.

20   Example 2:   Cosegregation Analysis for Lines with Lethal Phenotypes
            The linkage of the mutation to the *Ds* or T-DNA insertion is established after identifying a transformed line segregating for a lethal phenotype of interest. A line segregating with a single functional insert will segregate for resistance in the ratio of about 2:1 (resistant: sensitive) to the selectable marker. In the case of an embryo defective mutant,

25   one-quarter of the progeny of a plant heterozygous for an insertion will fail to germinate due to embryo lethality, resulting in a reduction of the normal 3:1 ratio to 2:1. In the case of a seedling lethal mutant, the seedlings with a mutant phenotype are excluded in the calculation of this ratio. Each of the resistant progeny is therefore heterozygous for the mutation if the *Ds* or T-DNA insertion is causing the mutant phenotype. To establish cosegregation of the

30   insertion and the mutant phenotype, about 30 resistant progeny are transplanted to soil and each plant is shown to segregate the 25% progeny with a lethal phenotype by the appropriate screening of embryo or seedlings. When all resistant plants segregate the lethal phenotype,

there is cosegregation of the insertion and the lethal mutation and the line is designated as "tagged."

Example 3:   T-DNA Border Isolation by Plasmid Rescue

5   The plasmid rescue technique is used to molecularly clone *Arabidopsis* flanking DNA from one or both sides of the T-DNA insertion(s). *Arabidopsis* genomic DNA is isolated as described by Reiter *et al.* in *Methods in Arabidopsis Research*, World Scientific Press (1992). Genomic DNA is digested with a restriction endonuclease and ligated overnight. After ligation, the DNA is transformed into competent *E. coli* strain XL-1 Blue, DH10B, DH5

10   alpha, or the like, and colonies are selected on semi-solid medium containing ampicillin. Resistant colonies are picked into liquid medium with ampicillin and grown overnight. Plasmid DNA is isolated and digested with the rescue enzyme and analyzed on agarose gels containing ethidium bromide for visualization. Plasmids that represent different size classes are sequenced using primers that flank the plant DNA portion of the rescue element and the

15   sequence is analyzed to determine what portion is plant DNA and what gene has been disrupted. The plasmid rescue is validated via PCR of template genomic DNA from a heterozygote for the insertion mutation. The experiment uses a primer anchored in the predicted flanking sequence and a primer in the T-DNA insertion. Finding a PCR product of the appropriate size, based on the sequence of the plasmid rescue clone confirms a valid

20   rescue. Alternatively, Southern blot analysis with a probe that detects the relevant region of *Arabidopsis* DNA in genomic DNA from a heterozygote for the insertion mutation can be used to confirm the plasmid rescue results.

Example 4:   Transposon or T-DNA Border Isolation by TAIL-PCR

25   *Arabidopsis* genomic DNA is isolated according to Reiter *et al.* in Methods in *Arabidopsis* Research, World Scientific Press (1992) or using the Nucleon PhytoPure™ Plant DNA isolation kit (Amersham International plc, Buckinghamshire, England) or the Puregene DNA isolation kit (Gentra Systems, Minneapolis, MN). Fragments of genomic DNA flanking the borders of the transposon or T-DNA are isolated using the TAIL-PCR technique (Liu *et*

30   *al.* (1995) Plant J., 8:457-463; Liu and Whittier (1995), Genomics, 25:674-681). Three sets of 12 TAIL-PCR reactions, referred to as the primary, secondary and tertiary reactions, are performed. In each reaction, one arbitrary degenerate primer and one transposon-specific or

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T-DNA-specific primer are used. The arbitrary degenerate primer is chosen from among seven primers, LWAD1, CA50, CA51, CA52, CA53, CA54, and CA55 (Table 1), which are used to prime the genomic DNA flanking the insertion. Alternatively, less than 12 TAIL-PCR reactions are done using fewer arbitrary degenerate primers. These degenerate primers

5   are used in combination with two sets of three, nested, transposon-specific primers (Table 2) or T-DNA-specific primers (Table 3). The transposon-specific primers are homologous to regions of the *Ds* elements that lie at the outermost ends of the transposons, DS5 at the 5' end (primers 5A, 5B, and 5C) and DS3 at the 3' end (primers 3A, 3B, and 3C). The T-DNA-specific primers are homologous to regions of the T-DNA that lie in the borders of the T-

10 DNAs. For the pCSA104 and pDAP101 T-DNAs, right borders are recovered with CA66 (primary primer), CA67 (secondary primer), and CA68 (tertiary primer) and left borders are recovered with JM33 (tertiary primer); JM34 (secondary primer); and JM35 (primary primer). For the pCSA110 T-DNA, right borders are recovered with QRB1 (primary primer), QRB2 (secondary primer), and QRB3 (tertiary primer) and left borders are recovered with JM33

15 (tertiary primer); JM34 (secondary primer); and JM35 (primary primer). For the pPCVICEn4HPT (Hayashi *et al.* (1992), Science, 258:1350-1353) and pSKI015 (Weigel *et al.* (2000) Plant Physiol. 122:1003-1014) T-DNAs, left borders are recovered with SKI1 (primary primer), SKI2 (secondary primer), and SKI3 (tertiary primer). When the degenerate and nested primer pairs are used in a series of low and high-stringency PCR amplifications, as

20 described in the TAIL-PCR protocol (Liu and Whittier (1995), Genomics, 25:674-681), DNA fragments are produced that correspond to the genomic DNA that is directly adjacent to the transposon or T-DNA insertion. The nucleic acid sequences of the PCR products from the tertiary TAIL-PCR reactions are then determined by standard molecular biology techniques. The resulting sequences are analyzed for the presence of non-*Ds* transposon or non-T-DNA

25 vector sequence.

        To confirm the integrity of the resultant products, PCR primers specific to the flanking genomic region are designed and used in conjunction with the tertiary nested primer in a PCR reaction, to confirm the transposon or T-DNA insertion point within the genomic DNA. Finding a PCR product of the appropriate size, based on the sequence of the TAIL-PCR clone

30 confirms a valid rescue.

Table 1: Arbitrary Degenerate Primers

SEQ ID NO:	Primer	Degen.	Primer Sequence
101	LWAD1	1026	ngt tgw gna twt sgw gnt
102	CA50	128	ngt cga swg ana wga a
103	CA51	128	tgw gna gsa nca sag a
104	CA52	128	agw gna gwa nca wag g
105	CA53	256	stt gnt ast nct ntg c
106	CA54	64	ntc gas twt sgw gtt
107	CA55	256	wgt gna gwa nca nag a

Table 2: Nested Primers For *Ds* Lines

SEQ ID NO:	Primer	Primer Sequence
108	5A	actagctctaccgtttccgtttccgtttac
109	5B	ttacctcgggttcgaaatcgatcgggataa
110	5C	aaaatcggttatacgataacggtcggtacggga
111	3A	gggtcttgcggatctgaatatatgttttcatgtgtg
112	3B	taccgaagaaaaataccggttcccgtccgatttcgac
113	3C	ggatcgtatcggttttcgattaccgtatttatcc

Table 3: Nested Primers For T-DNA Lines

SEQ ID NO:	Primer	Primer Sequence
114	CA66	att agg cac ccc agg ctt tac act tta tg
115	CA67	gta tgt tgt gtg gaa ttg tga gcg gat aac
116	CA68	taa caa ttt cac aca gga aac agc tat gac
117	JM33	tag cat ctg aat ttc ata acc aat ctc gat aca c
118	JM34	gct tcc tat tat atc ttc cca aat tac caa tac a
119	JM35	gcc ttt tca gaa atg gat aaa tag cct tgc ttc c
120	QRB1	caa act agg ata aat tat cgc gcg cgg tgt ca
121	QRB2	ggt gtc atc tat gtt act aga tcg gga att ga
122	QRB3	cgc cat ggc ata tgc tag cat gca taa ttc
123	SKI1	aat tgg taa tta ctc ttt ctt ttc ctc cat att ga
124	SKI2	ata ttg acc atc ata ctc att gct gat cca t
125	SKI3	tga tcc atg tag att tcc cgg aca tga a

Example 5:   Transposon or T-DNA Border Isolation by TAIL2k PCR

Arabidopsis genomic DNA is isolated according to Reiter *et al.* in <u>Methods in</u>

<u>Arabidopsis</u> Research, World Scientific Press (1992) or using the Nucleon PhytoPure™ Plant

5   DNA isolation kit (Amersham International plc, Buckinghamshire, England) or the Puregene

DNA isolation kit (Gentra Systems, Minneapolis, MN). Fragments of genomic DNA flanking

the borders of the transposon or T-DNA are isolated using the TAIL2k PCR technique. Two

sets of 12 TAIL-PCR reactions, referred to as the primary and secondary reactions, are

performed. In each reaction, one arbitrary degenerate primer and one transposon-specific or

10 T-DNA-specific primer are used. The arbitrary degenerate primer is selected from among six

primers; CA50, CA51, CA52, CA53, CA54, and CA55 (Table 1), which are used to prime the

genomic DNA flanking the insertion. Alternatively, less than 12 TAIL-PCR reactions are

done using fewer arbitrary degenerate primers. These degenerate primers are used in

combination with two sets of two, nested, transposon-specific primers (Table 2) or T-DNA-

15 specific primers (Table 3). The transposon-specific primers are homologous to regions of the

Ds elements that lie at the outermost ends of the transposons, DS5 at the 5' end (primers 5A,

5B, and 5C) and DS3 at the 3' end (primers 3A, 3B, and 3C). The T-DNA-specific primers

are homologous to regions of the T-DNA that lie in the borders of the T-DNAs. For the

pCSA104 and pDAP101 T-DNAs, right borders are recovered with CA66 (primary primer),

20 CA67 (secondary primer), and CA68 (sequencing primer) and left borders are recovered with

JM33 (sequencing primer), JM34 (secondary primer), and JM35 (primary primer). Primers

CA66, CA67, and CA68 are also known as RB1, RB2, and RB3, respectively. Primers JM35,

JM34, and JM33 are also known as LB1, LB2, and LB3, respectively. For the pCSA110 T-

DNA, right borders are recovered with QRB1 (primary primer), QRB2 (secondary primer),

25 and QRB3 (sequencing primer) and left borders are recovered with JM33 (sequencing

primer); JM34 (secondary primer); and JM35 (primary primer). For the pPCVICEn4HPT

(Hayashi *et al.* (1992), Science, 258:1350-1353) and pSKI015 (Weigel *et al.* (2000) Plant

Physiol. 122:1003-1014) T-DNAs, left borders are recovered with SKI1 (primary primer),

SKI2 (secondary primer), and SKI3 (sequencing primer). When the degenerate and nested

30 primer pairs are used in a series of low and high-stringency PCR amplifications, as described

in the TAIL-PCR protocol (Liu and Whittier (1995), Genomics, 25:674-681), DNA fragments

are produced that correspond to the genomic DNA that is directly adjacent to the transposon

or T-DNA insertion. TAIL2k-PCR differs from the original TAIL-PCR protocol by the elimination of the tertiary PCR and modification of the secondary PCR. The cycling conditions used in the secondary reaction are modified to include 5 high annealing temperature cycles (64 degrees C) at the beginning, three additional so-called super cycles,

5   and five additional low annealing temperature cycles (44 degrees C) at the end of the reaction. The melting and extension times are the same as all other TAIL-PCR reactions. Additionally, the reaction volume is increased to 40 microliters. The nucleic acid sequences of the PCR products from the secondary TAIL2k-PCR reactions are then determined by standard molecular biology techniques. The resulting sequences are analyzed for the presence of non-

10 *Ds* transposon or non-T-DNA vector sequence.

        To confirm the integrity of the resultant products, PCR primers specific to the flanking genomic region are designed and used in conjunction with the tertiary nested primer in a PCR reaction, to confirm the transposon or T-DNA insertion point within the genomic DNA. Finding a PCR product of the appropriate size, based on the sequence of the TAIL2k-PCR

15 sequencing result confirms a valid rescue.

        Example 6:   Identification of Both Borders of a T-DNA or *Ds* Insertion
        If the results of border rescue provide information on only one of the two borders for an insertion in a given line, additional experiments are performed to identify the second

20 border. These experiments are necessary to show that a single gene has been disrupted in a given line. In some cases, an insertion can affect more than a single gene due to a chromosomal deletion or rearrangement. In those cases, additional experiments are required to identify which of the affected genes is responsible for the lethal phenotype.

        When both borders of an insertion are not recovered, primers are designed to isolate a

25 PCR product that will provide information on the location of the missing border. Three primers are chosen in *Arabidopsis* genomic DNA on the opposite side of the insertion about one, two, and five kb away from the insertion point; the primers point towards the expected second border. Long PCR conditions (Advantage 2, Clontech) are then employed following the manufacturer's directions to amplify the relevant region from genomic DNA isolated from

30 a heterozygote for the lethal mutation. PCR reactions are performed using appropriate pairs of genomic and T-DNA or *Ds* border primers. Finding a PCR product of the appropriate size,

based on the sequence of the TAIL-PCR clone confirms a valid rescue of the second border. In some cases, the PCR product is directly sequenced to determine the exact insertion point.

If the second border is not recovered with this method, an additional set of PCR reactions are preformed. In these experiments, the genomic primers are paired with a series of

5   internal T-DNA or *Ds* primers designed at about one kb intervals in both orientations across the entire T-DNA or *Ds* vector sequence. Finding a PCR product of the appropriate size, based on the sequence of the TAIL-PCR clone confirms a valid rescue of the second border. In some cases, the PCR product is directly sequenced to determine the exact insertion point. Any borders recovered with this approach are classified as abnormal because they lack the

10   ends of the *Ds* transposon or the expected 24 bp T-DNA imperfect repeat characteristic of right and left borders.

Example 7:   Identification of Insertion Points for Lines with Lethal Phenotypes

For each line with a lethal phenotype, the sequences of the borders of the insertion are

15   determined and the insertion points in the *Arabidopsis* genome are deduced. For *Ds* insertion lines, PCR products are obtained from the Ds3 and Ds5 borders. For T-DNA lines, PCR products or plasmid rescue clones are obtained from left (LB), right (RB), or abnormal (AB) borders. These sequences are used in BLASTn searches against nucleotide databases (Altschul *et al.* (1990) J Mol. Biol. 215:403-410; Altschul *et al.* (1997) Nucleic Acids Res.

20   25:3389-3402). The results are summarized in Table 4. *Ds* line names begin with ET or GT; T-DNA line names are numbers. The insertion point (Insert Pt.) and the direction of the flanking sequence (Dir.) either up (U) or down (D) in the genome section is noted. Often, small deletions or duplications of genomic DNA accompany the insertion of a T-DNA or *Ds* transposon.

25   The gene that has been inactivated in a given line with a lethal phenotype is determined from the insertion points for that line. Often, the precise location of an ORF for a given gene is not known, but predictions are available in genome sections deposited in GenBank. The precise boundaries of that ORF is determined as described in Example 7.

30   Table 4: Insertion Points For Lines With Lethal Phenotypes

Gene	Line #	Border	Genome Section	Acc. #	Insert Pt.	Dir.
942	942	LB	K24G6	AB012242	33667	D

978	978	LB	F23N20	AC016972	58221	D
	978	LB	F23N20	AC016972	58301	U
3218	3218	LB	T8K14	AC007202	10500	D
	3218	LB	T8K14	AC007202	10540	U
4563	4563	LB	ATCHRII092	AC006438	25542	D
8794	8794	LB	F2J6	AC009526	45854	D
	8794	LB	F2J6	AC009526	45879	U
9106	9106	LB	T2J13	AL132967	78013	U
	9106	AB	T2J13	AL132967	77943	D
10708	10708	RB	F1I21	AC005687	40005	D
	10708	LB	F1I21	AC005687	40042	U
	70241	LB	F1I21	AC005687	40210	D
	70241	RB	F1I21	AC005687	40215	U
10844	10844	LB	F13F21	AC007504	60873	U
	10844	LB	F13F21	AC007504	60839	D
10951	10951	LB	MKP11	AB005238	20298	D
	10951	LB	MKP11	AB005238	20318	U
12935	12935	LB	ATCHRII150	AC005168	36510	D
	12935	LB	ATCHRII150	AC005168	36545	U
13823	11361	LB	T27G7	AC006932	78096	U
	11361	AB	T27G7	AC006932	78065	D
	13823	LB	T27G7	AC006932	78096	U
	13823	RB	T27G7	AC006932	77722	D
14519	14519	LB	ATCHRIV72	AL161576	50259	U
	14519	AB	ATCHRIV72	AL161576	50228	D
14610.1	14610.1	LB	F4P13	AC009325	55319	U
	14610.1	RB	F4P13	AC009325	55442	D
14891	14891	LB	ATCHRIV89	AL161593	11412	U
	14891	RB	ATCHRIV89	AL161593	11313	D
14986	14986	LB	K10D20	AP000410	51816	D
	14986	RB	K10D20	AP000410	54505	U
15377	15377	RB	F28G11	AC074025	19572	D
	15377	LB	F28G11	AC074025	19587	U
16219	16219	LB	MRO11	AB005244	51998	U
	16219	LB	MRO11	AB005244	51995	D
16547	16547	LB	ATCHRIV65	AL161565	80692	D
	16547	RB	ATCHRIV65	AL161565	80791	U
20933	20933	LB	ATCHRII146	AC004747	47678	D
	20933	LB	ATCHRII146	AC004747	47683	U
21455	21455	LB	ATCHRIV54	AL161554	105596	U
	21455	RB	ATCHRIV54	AL161554	105542	D
21878	21878	LB	T19F11	AC009918	19609	D
23915	23915	LB	ATCHRII008	AC005936	49629	D
	23915	LB	ATCHRII008	AC005936	49657	U
30945	30945	LB	ATCHRII192	AC004238	2411	D
	30945	LB	ATCHRII192	AC004238	2410	U

31895	31895	LB	MTI20	AB013396	52020	D
	31895	LB	MTI20	AB013396	52089	U
34269	34269	LB	T4O12	AC007396	92811	U
	34269	RB	T4O12	AC007396	92808	D
34540	34540	LB	T1G11	AC002376	41572	D
	34540	LB	T1G11	AC002376	41608	U
	72902	LB	T1G11	AC002376	41494	U
	72902	LB	T1G11	AC002376	41465	D
34555	34555	LB	T1F15	AC004393	42152	D
	54334	RB	T1F15	AC004393	41803	U
	54334	LB	T1F15	AC004393	41671	D
35154	35154	RB	MWD9	AB007651	45718	D
	35154	LB	MWD9	AB007651	45732	U
35438	35438	LB	MAL21	AP000383	25170	D
	35438	LB	MAL21	AP000383	25738	U
37351	37351	LB	F25C20	AC007296	52890	U
	37351	RB	F25C20	AC007296	52196	D
37389	37389	LB	F3F19	AC007357	45488	U
	37389	RB	F3F19	AC007357	45471	D
38108	38108	LB	ATCHRII150	AC005168	83430	D
	38108	RB	ATCHRII150	AC005168	83446	U
43301	43301	RB	T22D16	AL357612	57549	D
	43301	LB	T22D16	AL357612	57599	U
46250	46250	LB	F17A9	AC016827	74222	D
	46250	RB	F17A9	AC016827	74274	U
47050A	47050	LB	T23E18	AC009978	49445	D
	47050	RB	T23E18	AC009978	49475	U
52949A	52949	LB	K16H17	AB016884	34713	D
	52949	LB	K16H17	AB016884	34718	U
53210A	53210	RB	ATCHRII017	AC007167	92796	D
	53210	LB	ATCHRII017	AC007167	92942	U
	69121	LB	ATCHRII017	AC007167	94478	D
	69121	LB	ATCHRII017	AC007167	94502	U
55483	55483	RB	ATCHRII164	AC005727	71269	U
	55483	LB	ATCHRII164	AC005727	71258	D
58351A	58351	RB	MYH9	AB016893	42547	D
	58351	LB	MYH9	AB016893	42772	U
60944	60944	LB	F1B16	AC023754	89492	U
	60944	LB	F1B16	AC023754	89428	D
62837	62837	LB	T21J18	AL132963	70906	U
	62837	LB	T21J18	AL132963	70873	D
65310	65310	LB	T20H2	AC022472	8158	U
	65310	RB	T20H2	AC022472	8096	D
68181	68181	RB	F12A12	AL133314	38270	U
	68181	LB	F12A12	AL133314	38275	D
70913	70913	LB	T24H18	AL353013	5347	D

	70913	LB	T24H18	AL353013	5358	U
71067	71067	LB	F2E2	AC069252	63031	U
	71067	LB	F2E2	AC069252	62932	D
71654	71654	RB	MYA6	AB023046	71956	U
	71654	LB	MYA6	AB023046	71907	D
ET3172	ET3172	DS5	ATCHRIV4	AL161492	134442	U
ET3546	ET3546	DS3	ATCHRII15	AC006081	20874	D
	ET3546	DS5	ATCHRII15	AC006081	20973	U

Example 8:   Identification of cDNAs for Essential Genes

A cDNA for a gene identified as essential is identified using a variety of approaches. This information enables the ORF for a given gene to be identified and used for other

5   experiments including expression of the corresponding protein in heterologous systems.

If there is a full-length cDNA deposited in GenBank or published elsewhere, that sequence may be checked independently using methods described below. Alternatively, the sequence may be considered to be correct.

In some cases, there are published EST sequences that can be assembled to cover the

10   entire ORF from start codon to stop codon. This sequence may be checked independently using methods described below or it may be considered to be correct.

Often part of the cDNA is published and this information can be used to identify the entire ORF. If the 5' end containing the start codon is known, 3' RACE is performed to identify the remainder of the cDNA. If the 3' end containing the stop codon is known, 5'

15   RACE is performed to identify the remainder of the cDNA. If both the 5' and the 3' ends are known, but the sequence between the two ends of the cDNA is not known, PCR is performed with primers hybridizing to each end of the cDNA. In all three of these cases, PCR is performed using template DNA from a GeneRacer (Invitrogen) or a Marathon (Clontech) cDNA library prepared from RNA isolated from seedling tissue. A resulting PCR product is

20   TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced.

If no part of the cDNA is published, the cDNA is identified by starting from gene model predictions in the annotation for genomic clones or elsewhere. To identify the ORF, primers are designed to the 5' and 3' ends of the predicted ORF. PCR is performed using template DNA from a cDNA library prepared from seedling tissue or the pFL61 *Arabidopsis*

25   cDNA library (Minet *et al.* (1992) Plant J. 2: 417-422). The resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced. Alternatively, 5' and 3' RACE are performed with primers predicted by gene models to be in exons. PCR is performed using

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template DNA from a GeneRacer (Invitrogen) or a Marathon (Clontech) cDNA library prepared from RNA isolated from seedling tissue. A resulting PCR product is TA-cloned (Original TA-Cloning kit, Invitrogen) and sequenced.

If the cDNA sequence is the same as the sequence predicted in the GenBank
5   annotation, the experiments confirm for the first time the actual ORF. If the cDNA sequence is not the same as the sequence predicted in the GenBank annotation, the experiments identify for the first time the actual ORF. In some cases, more than one cDNA sequence is found for a given gene and both sequences are included in this application.

10   Example 9:   Description of Essential Genes

The putative function of the protein encoded by each essential gene is determined from analysis of the ORF in each cDNA. Information from the relevant *Arabidopsis* genomic section deposited in GenBank is used as a starting point to explore the function of a given gene. This analysis also includes BLAST searches (Altschul *et al.* (1990) J. Mol. Biol.
15   215:403-410; Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-3402) of sequence databases to identify similar proteins. Table 5 describes the putative functions for the essential genes discovered in this application.

Table 5: Putative Functions For Essential Genes

20

Gene	SEQ ID Nos:	Putative Function & Similar Genes	References
00942	1-2	similarity to disease resistance protein large gene family in *Arabidopsis* including disease resistance proteins RPP1-WsA,B&C; similar to tobacco TMV resistance protein N	Whitham, S. *et al.* (1994) Cell 78:1101-1115; Botella, M.A., *et al.* (1998) Plant Cell 10: 1847-1860
00978	3-4	unknown protein similar to *Arabidopsis* protein of unknown function (CAB87660) & ESTs from many plants	none
03218	5-6	AAA ATPase similar to *E. coli* FtsH cell division protein (P28691) that acts as an ATP-dependent metallopeptidase; homologs in many species	Schumann, W. (1999) FEMS Microbiol Rev 23:1-11; Langer, T. (2000) Trends Biochem Sci 2000 25:247-251

04563	7-8	unknown protein large gene family in *Arabidopsis* of unknown function proteins	none
08794	9-10	putative histidine decarboxylase similar to Brassica, tomato (tom92), and rice putative histidine decarboxylases	Picton, S et al. (1993) *Plant Mol Biol* 23:627-631; Watanabe, T et al. (1990) Trends Pharmacol Sci 11:363-367; Vaaler, G.L. & Snell, E.E. (1989) Biochemistry 28:7306-7313
09106	11-12	cytosolic 40S ribosomal protein S11-alpha	Browning, K.S. (1996) *Plant Mol Biol* 32:107-144; Gantt, J. S. & Thompson, M.D. (1990) *J. Biol Chem* 265:2763-2767
10708	13-14	cytoplasmic 60S ribosomal protein L3	Peltz, S.W. et al. (1999) *Mol Cell Biol* 19:384-391; Kim, Y. et al. (1990) *Gene* 93:177-182; Wickner, R.B et al. (1982) *Proc Natl Acad Sci USA* 79:4706-4708
10844	15-16	40S ribosomal protein S17-like	Gantt, J.S. & Thompson, M.D. (1990) *J Biol Chem* 265:2763-2767; Wiener, L. et al. (1988) *Nucleic Acids Res* 16:1233-1250
10951	17-18	phytoene synthase	Welsch, R. et al. (2000) *Planta* 211:846-854; Shewmaker, C.K. et al. (1999) *Plant J.* 20:401-412; Von Lintig, J. et al. (1997) *Plant J.* 12:625-634
12935	19-20	putative choline kinase similar to soybean choline kinase (T08815) and mouse & human choline/ethanolamine kinases	Monks, D.E. et al. (1996) Plant Physiol. 110:1197-1205; Bligny, R. et al. (1989) J Biol Chem. 264:4888-4895; Wharfe, J. & Harwood, J.L. (1979) Biochim Biophys Acta. 575:102-111
13823	21-22	magnesium protoporphyrin IX chelatase subunit D	Papenbrock, J. et al. (1997) Plant J. 12:981-990; Papenbrock, J. et al. (2000) Plant Physiol. 122:1161-1169; Luo, M. et al. (1999) Plant Mol Biol. 41:721-731; Jensen, P.E. et al. (1996) Mol. Gen. Genet. 250:383-394

14519	23-24	putative protein small gene family in *Arabidopsis* of unknown function proteins	none
14610.1	25-26	putative cell division control protein; similar to cdc48, AAA ATPase proteins similar to *S. pombe* AAA ATPase (CAB16902); *Arabidopsis* cdc48 homolog (P54609); cdc48/valosin-containing protein homologs from soybean, *Capsicum annuum*, rice, Dictylostelium; Drosophila smallminded	Frohlich, K.U. *et al.* (1991) J Cell Biol. 114:443-453; Feiler, H.S. *et al.* (1995) EMBO J. 14:5626-5637; Langer, T. (2000) Trends Biochem Sci 2000 25:247-251
14891	27-28	putative protein contains PFAM 02536 mTERF (mitochondrial transcription termination factor) domain; large gene family in *Arabidopsis* of unknown function proteins	Fernandez-Silva, P. *et al.* (1997) EMBO J 16:1066-1079
14986	29-30	ubiquitin isopeptidase T (aka ubiquitin-specific protease 14)	Wilkinson, K.D. *et al.* (1995) Biochemistry 34:14535-14546; Falquet, L. *et al.* (1995) FEBS Lett 376:233-237; Lindsey, D.F. *et al.* (1998) J Biol Chem 273:29178-29187
15377	31-32	putative formyl transferase similar to *B. napus* methionyl tRNA transformylase Fmt protein (AJ245479) & *B. rapa* S-locus protein 8 (AB022076)	Cui Y *et al.* (1999) Plant Cell. 11:2217-2231; Suzuki, G. *et al.* (1999) Genetics 153:391-400; Cusack S. (1999) Curr Opin Struct Biol. 9:66-73
16219	33-34	polyadenylation cleavage/specificity factor 100 kDa subunit (AF283277)	Bilger, A. *et al.* (1994) Genes Dev. 8:1106-1116; Bienroth, S. *et al.* (1993) EMBO J. 12:585-594; Jenny, A. *et al.* (1994) Mol Cell Biol. 14:8183-8190
16547	35-36	similarity to UV-induced protein Uvi31, *S. pombe*, G1381578 unknown function, but similar to Pectobacterium chrysanthemi SufE protein (AJ301654) involved in iron metabolism, *S. pombe* uvi31 protein of the BolA / YRBA family (Q12238), Synechocystis hypothetical 17.7 KDA protein SLR1419 (P74523)	Kim, S.H. *et al.* (1997) Environ Mol Mutagen 30:72-81; Santos, J.M. *et al.* (1999) Mol Microbiol 32:789-798

20933	37-38	hypothetical protein contains WD40 repeats, similar to human CIAO 1 gene (O76071) & S. cerevisiae YDR267c (S70127)	Neer, E.J. et al. (1994) Nature 371:297-300; Johnstone, R.W. et al. (1998) J Biol Chem 273:10880-10887
21455	39-40	putative protein small gene family in Arabidopsis of unknown function proteins	none
21878	41-42	Arabidopsis digalactosyldiacylglycerol synthase (DGD1, AAD42378)	Dormann, P. et al. (1999) Science 284:2181-2184; Hartel, H. et al. (1997) Plant Physiol 115:1175-1184
23915	43-44	hypothetical protein contains PPR motifs, member of large gene family in Arabidopsis	Small, I.D. & Peeters, N. (2000) Trends Biochem Sci 25:46-47; Manthey, G.M. & McEwen, J.E. (1995) EMBO J 14:4031-4043; Barkan, A. et al. (1994) EMBO J 13:3170-3181
30945	45-46	unknown protein similar to rice hypothetical protein (BAB56056)	none
31895	47-48	similar to unknown protein small gene family in Arabidopsis of unknown function proteins	none
34269	49-50	unknown protein	none
34540	51-52	probable lipoate protein ligase B, similar to Mycobacterium LIPB gene (O32961) also similar to S. pombe putative pre-tRNA/pre-rRNA processing protein (T41635)	Reed, K.E. & Cronan, J.E. Jr. (1993) J Bacteriol 175:1325-1336; Chen, X.J. (1997) Mol. Gen. Genet. 255:341-349
34555	53-54	similar to Synechocystis hypothetical 41.9KD protein (P52640) similar to several prokaryotic proteins of unknown function including E. coli YJEQ (P39286)	none
35154	55-56	similar to unknown protein similar to human hypothetical protein (BAA91556), S. cerevisiae probable membrane protein YOR262w (S67159), & S. pombe ATP(GTP)-binding protein Fet5 (AAC49837)	Shpakovskii, G.V. & Lebedenko, E.N. (1997) Bioorg. Khim. 23:234-237
35438	57-58	unknown protein weak similarity to Pennisetum ciliare unknown function protein (AAK15504)	none

37351	59-60	strong similarity to obtusifoliol 14-alpha demethylase (CYP51; P93846) from Sorghum bicolor (also wheat & rice), member of the PF00067 cytochrome P450 family	Kushiro, M. *et al.* (2001) Biochem Biophys Res Commun. 285:98-104; Bak *et al.* (1997) Plant J. 11:191-201; Grausem, B. (1995) Plant J. 7:761-770
37389	61-62	similar to human GLE1-like required for poly(A)+ RNA export (AAC25561)	Watkins, J.L. *et al.* (1998) Proc. Natl. Acad. Sci. U.S.A. 95:6779-6784; Murphy, R. & Wente, S.R. (1996) Nature 383:357-360
38108	63-64	*Arabidopsis* 4-(cytidine 5'-phospho)-2-C-methyl-D-erythritol kinase (aka ispE & 4-diphosphocytidyl-2-C-methyl-Derythritol kinase) (AF288615) similar to *E. coli* ychB (aka ispE) gene (P24209)	Rohdich, F. *et al.* (2000) Proc Natl Acad Sci U.S.A. 97:8251-8256; Luettgen, H. *et al.* (2000) Proc. Natl. Acad. Sci. U.S.A. 97:1062-1067; Lange, B.M. & Croteau, R. (1999) Proc Natl Acad Sci U.S.A. 96:13714-13719
43301	65-66	similar to hypothetical bacterial proteins, including *Pseudomonas aeruginosa* protein PA0292 (F83608) & *Lactococcus lactis* (AAK05795)	none
46250	67-68	hypothetical protein weak similarity to hypothetical proteins from *Arabidopsis* (AAG51506) and mouse (BAB23375)	none
47050A	69-70	unknown protein weak similarity to Botrytis cDNA (AL115827)	none
52949A	71-72	6-phosphogluconolactonase-like protein similar to 6-phosphogluconolactonases such as human (O95336), Brassica carinata (AAK50346), & *Mycobacterium tuberculosis* (devB, CAB09261)	Collard, F. *et al.* (1999) FEBS Lett. 459:223-226; Bauer, H.P. *et al.* (1983) Eur J Biochem. 133:163-168
53210A	73-74	putative heat shock protein in hsp90 family similar to rye hsp82 (S65776), Ipomoea nil hsp83 (P51819), chicken hsp90 beta (Q04619) and others	Felsheim, R.F. & Das, A. (1992) Plant Physiol. 100:1764-1771; Coates, A.R. *et al.* (1999) *Biotechnol Genet Eng Rev* 16:393-405; Milioni, D. & Hatzopoulos, P. (1997) *Plant Mol Biol* 35:955-961

55483	75-76	putative para-aminobenzoate synthase and glutamine amidotransferase, a bifunctional enzyme similar to *Streptomyces pristinaespiralis* papA (AAC44866), *E. coli* pabB (P05041) & pabA (P00903), and *Bacillus stearothermophilus* anthranilate synthase component I trpE (AAD33791)	Goncharoff, P. & Nichols, B.P. (1984) J Bacteriol. 159:57-62.; Roux, B. & Walsh, C.T. (1992) Biochemistry. 31:6904-6910; Kaplan, J.B. & Nichols, B.P. (1983) J Mol Biol 168:451-468
58351A	77-78	26S proteasome p55 protein-like similar to human 26S proteasome regulatory complex chain p55 (BAA19749), *S. cerevisiae* 26S proteasome regulatory complex chain RPN5 (S67695), and others	Saito, A. *et al.* (1997) *Gene* 203:241-250; Glickman, M.H. *et al.* (1998) Mol Cell Biol 18:3149-3162
60944	79-80	similar to Guillardia theta chloroplast 50S ribosomal protein L31 (O46917)	Yamaguchi, K. & Subramanian, A.R. (2000) *J Biol Chem*, 275:28466-28482
62837	81-82	AtClpC: regulatory subunit of Clp protease with ATPase activity (BAA82062)	Adam, Z. (2000) Biochimie 82:647-654; Sokolenko, A. *et al.* (1998) Planta 207:286-295; Nakabayashi, K. *et al.* (1999) Plant Cell Physiol. 40:504-514; Maurizi, M.R. *et al.* (1990) J Biol Chem. 265:12536-12545
65310	83-84	26S proteasome regulatory subunit S3, contains a PCI PF01399 domain similar to 26S proteasome regulatory subunit S3 from Nicotiana tabacum (P93768), carrot (Q06364), human (O43242), *S. cerevisiae* RPN3 (P40016), and others	Voges, D. *et al.* (1999) Ann Rev Biochem 68:1015-1068; Fu, H. *et al.* (1999) Mol Biol Rep 26:137-146; Fu, H. *et al.* (1999) Plant J 18:529-539; Kominami, K. *et al.* (1997) Mol Biol Cell 8:171-187
68181	85-86	small zinc finger-like protein TIM9 similar to mitochondrial import inner membrane translocase subunit TIM9 from several plants and *S. cerevisiae* (O74700)	Koehler, C.M. *et al.* (1998) EMBO J. 17:6477-6486; Tokatlidis, K. *et al.* (2000) Biochem Soc Trans 28:495-499
70913	87-88	*Arabidopsis* CCAAT binding protein/transcription factor Hap2a (CAA74048)	Edwards, D. *et al.* (1998) Plant Physiol 117:1015-1022; Albani, D. & Robert, L.S. (1995) *Gene* 167:209-213

71067	89-90	hypothetical protein gene family in *Arabidopsis* of unknown function proteins	none
71654	91-92	poly(A) binding protein-like	Hilson, P. *et al.* (1993) *Plant Physiol* 103:525-533; Belostotsky, D.A. & Meagher, R.B. (1993) *Proc Natl Acad Sci U.S.A.* 90:6686-6690; Gallie, D.R. (1998) *Gene* 216:1-11
ET3172	93-94	hypothetical protein small gene family in *Arabidopsis* (T47999 & T02193) of unknown function	none
ET3546	95-96	cdc27/nuc2-like protein, may contain TPR-repeat similar to human cdc27 (P30260), *S. pombe* nuc2 (P10505), *S.* *cerevisiae* cdc23 (P16522), and others	Hirano, T. *et al.* (1988) J. Cell Biol. 106:1171-1183; Chen, P.L. *et al* (1995) Cell Growth Differ. 6:199-210

Example 10:   Expression of Recombinant Essential Proteins in *E. coli*

The coding region of each of the essential proteins, corresponding to cDNA clones of odd-numbered SEQ ID NO:1-96, is subcloned into an appropriate expression vector, and transformed into *E. coli* using the manufacturer's conditions. Specific examples include plasmids such as pBluescript (Stratagene, La Jolla, CA), pFLAG (International Biotechnologies, Inc., New Haven, CT), and pTrcHis (Invitrogen, La Jolla, CA). *E. coli* is cultured, and expression of the essential protein is confirmed. Recombinant protein is isolated using standard techniques.

Example 11:   *In Vitro* Binding Assays

Recombinant protein for each of the essential genes described in this application is obtained, for example, according to Example 10. The protein is immobilized on chips appropriate for ligand binding assays using techniques that are well known in the art. The protein immobilized on the chip is exposed to sample compound in solution according to methods well know in the art. While the sample compound is in contact with the immobilized protein, measurements capable of detecting protein-ligand interactions are conducted. Examples of such measurements are SELDI, biacore and FCS, described above. Compounds

-38-

found to bind the protein are readily discovered in this fashion and are subjected to further characterization.

5   The above-disclosed embodiments are illustrative. This disclosure of the invention will place one skilled in the art in possession of many variations of the invention. All such obvious and foreseeable variations are intended to be encompassed by the present invention.

CLAIMS:

1. A method of identifying a herbicidal compound, comprising:

   a) combining a polypeptide comprising an amino acid sequence at least 90% identical
      to an amino acid sequence selected from the group consisting of the even
      numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to bind
      to said polypeptide, under conditions conducive to binding;

   b) selecting a compound identified in (a) that binds to said polypeptide;

   c) applying a compound selected in (b) to a plant to test for herbicidal activity; and

   d) selecting a compound identified in (c) that has herbicidal activity.

2. The method according to claim 1, wherein said polypeptide comprises an amino acid
sequence at least 95% identical to an amino acid sequence selected from the group consisting
of the even numbered SEQ ID NOs:2-96.

3. The method according to claim 2, wherein said polypeptide comprises an amino acid
sequence at least 99% identical to an amino acid sequence selected from the group consisting
of the even numbered SEQ ID NOs:2-96.

4. The method according to claim 3, wherein said polypeptide comprises an amino acid
sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

5. A method of identifying a herbicidal compound, comprising:

   c) combining a polypeptide comprising an amino acid sequence at least 90% identical
      to an amino acid sequence selected from the group consisting of the even
      numbered SEQ ID NOs:2-96 with a compound to be tested for the ability to inhibit
      the activity of said polypeptide, under conditions conducive to inhibition;

   d) selecting a compound identified in (a) that inhibits the activity of said polypeptide;

   c) applying a compound selected in (b) to a plant to test for herbicidal activity; and

   d) selecting a compound identified in (c) that has herbicidal activity.

-40-

6.   The method according to claim 5, wherein said polypeptide comprises an amino acid sequence at least 95% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

5   7.   The method according to claim 6, wherein said polypeptide comprises an amino acid sequence at least 99% identical to an amino acid sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

8.   The method according to claim 7, wherein said polypeptide comprises an amino acid
10   sequence selected from the group consisting of the even numbered SEQ ID NOs:2-96.

9.   A method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to the method of claim 1.

15   10.   A method for killing or inhibiting the growth or viability of a plant, comprising applying to the plant a herbicidal compound identified according to the method of claim 5.

SEQUENCE LISTING

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AND DEVELOPMENT AND USES THEREOF

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65                  70                  75                  80
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gta aga aaa caa att ggg aaa ctg tac gaa gca ttc tca ttg cat gag      384
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aga gaa aac cct gaa aag gtt caa aca tgg agg caa gca ctg tcc caa      432
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```

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                    165                 170                 175
```

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            195                 200                 205
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225                 230                 235                 240
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                    245                 250                 255
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Ala Glu Tyr Val Cys Leu Arg Leu Glu Lys Ala Arg Thr Leu Ser Lys
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2

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cta tac gaa tac agc tct atc atg gaa act ttt tca agt caa ccg att   1296
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atg caa gct ttg tcg gca ttg tta gag cta gaa tcc gac aaa gaa gtt   1392
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ttt cta gaa aat gct caa gag agc agt tca tcc tgt cta gaa gaa cgg   1536
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Ala Ser Lys Ser Ser Asp Leu Cys Gly Leu Val Gly Met Asp Arg His
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Met Lys Ala Met Tyr Arg Leu Leu Asp Leu Gly Leu Lys Asp Glu Val
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Ser Ser Thr Thr Arg Ser Phe Glu Asp Leu Val Gly Met Asn His Arg
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Ser Arg Tyr Ala Tyr Glu Arg Ile Ser Gln Gln Phe His Thr His Ala
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6

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Ala Arg Asp Glu Ser Phe Leu Leu Ala Ser Gly Val Lys Tyr Ile Phe
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Glu Val Lys Gly Leu Arg Phe Asp Gln Ala Leu Gln Leu Phe Tyr Gln
        595             600             605


Phe Ala Phe Lys Gln Lys Ser Pro Pro Val Arg Phe Arg Gln Leu Ser
        610             615             620


Val Arg Ala Ile Lys Leu Val Gly Phe Leu Pro Leu Ala Leu Lys Val
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Trp	Asp	Arg	Leu	Pro	Met	Thr	Ile	Ala	Phe	Thr	Ser	Ile	Met	Ala	Ile	
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tat	tgg	cta	tgg	gct	gca	ggg	ttc	tat	ctc	tta	gcc	aag	gtg	gaa	gaa	624
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gct	gcg	gat	aag	cct	ata	tat	agc	tgg	act	cat	cat	att	att	agt	ggg	672
Ala	Ala	Asp	Lys	Pro	Ile	Tyr	Ser	Trp	Thr	His	His	Ile	Ile	Ser	Gly	
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Lys Thr Trp Lys Lys Gly Ser Glu Glu Glu Arg Phe Glu His Ser Tyr
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Phe Gly Ser Ser Tyr Tyr His Leu His Pro Asn Asp Ala Thr Leu Leu
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Ile Pro Leu Met Ala Ile Leu Leu Pro Pro Met Tyr Thr His Ser Thr
            180             185             190


Tyr Trp Leu Trp Ala Ala Gly Phe Tyr Leu Leu Ala Lys Val Glu Glu
        195             200             205


Ala Ala Asp Lys Pro Ile Tyr Ser Trp Thr His His Ile Ile Ser Gly
    210             215             220


His Ser Leu Lys His Leu Cys Ala Ala Met Val Pro Val Phe Leu Thr
225             230             235             240


Leu Met Leu Ala Lys Arg Thr Val Gln Thr Glu Arg Ile Ser Leu Tyr
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Lys Thr Trp Lys Lys Gly Ser Glu Glu Glu Arg Phe Glu His Ser Tyr
            260             265             270


Ser Asn Val Ala Val Glu Glu Thr Arg
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atg gag att gca att tcg tat aaa ccg aat ccg ctt atc tct tca tcg        48
```

```
Met Glu Ile Ala Ile Ser Tyr Lys Pro Asn Pro Leu Ile Ser Ser Ser
1               5               10              15
```

```
act cag ttg ttg aaa aga tca aaa agt ttt ggt ctt gtt cgg ttt ccc         96
Thr Gln Leu Leu Lys Arg Ser Lys Ser Phe Gly Leu Val Arg Phe Pro
            20              25              30
```

```
gcc aag tat gga ctg gga gct acc cgg aaa aaa cag ctc ttt cga gtc        144
Ala Lys Tyr Gly Leu Gly Ala Thr Arg Lys Lys Gln Leu Phe Arg Val
            35              40              45
```

```
tat gcg tct gaa agt agt agt ggg tct tca tct aat agc gat gga ggc        192
Tyr Ala Ser Glu Ser Ser Ser Gly Ser Ser Ser Asn Ser Asp Gly Gly
        50              55              60
```

```
ttt tcg tgg gtg aga ttg gct cag tct att cgc ctt ggt gcc gag cgg        240
Phe Ser Trp Val Arg Leu Ala Gln Ser Ile Arg Leu Gly Ala Glu Arg
65              70              75              80
```

```
att ggg gag aag att gga gaa tct gtg aag aca gaa att ggg ttt gac        288
Ile Gly Glu Lys Ile Gly Glu Ser Val Lys Thr Glu Ile Gly Phe Asp
                85              90              95
```

```
tcg gaa gaa gca agt ggg aga gtg aat gag tat gtg gct cga gtt aag        336
Ser Glu Glu Ala Ser Gly Arg Val Asn Glu Tyr Val Ala Arg Val Lys
            100             105             110
```

```
gat agt gtg cac aag ggc cat cac gag ctg act cgc ttt aag aat gag        384
Asp Ser Val His Lys Gly His His Glu Leu Thr Arg Phe Lys Asn Glu
            115             120             125
```

```
aca gtg cct tcg ttt att gat tgg aac aag tgg gag cat tgg aag gac        432
Thr Val Pro Ser Phe Ile Asp Trp Asn Lys Trp Glu His Trp Lys Asp
            130             135             140
```

```
atc agg aat tgg gac ggt aaa cga gtt gct gcc ttg ttc ata tat gct        480
Ile Arg Asn Trp Asp Gly Lys Arg Val Ala Ala Leu Phe Ile Tyr Ala
145             150             155             160
```

```
ttt gcg ctg tta ctt tct tgt caa aga gtt tat gtt gcc atc caa gct        528
Phe Ala Leu Leu Leu Ser Cys Gln Arg Val Tyr Val Ala Ile Gln Ala
            165             170             175
```

```
cct cgg gta gaa cga gag aga aga gag tta aca gag tct ttt atg gag        576
Pro Arg Val Glu Arg Glu Arg Arg Glu Leu Thr Glu Ser Phe Met Glu
            180             185             190
```

```
gct ttg atc ccc gag cca tct cct gga aat ata gaa aag ttc aag aga        624
Ala Leu Ile Pro Glu Pro Ser Pro Gly Asn Ile Glu Lys Phe Lys Arg
            195             200             205
```

```
aat atg tgg agg aaa gca aca cct aaa ggc ttg aaa tta aaa agg ttc        672
Asn Met Trp Arg Lys Ala Thr Pro Lys Gly Leu Lys Leu Lys Arg Phe
            210             215             220
```

```
att gaa gcg cct gat gga aca ctt gtc cac gat agt tct tat gtt gga        720
Ile Glu Ala Pro Asp Gly Thr Leu Val His Asp Ser Ser Tyr Val Gly
225             230             235             240
```

```
gaa aat gcg tgg gat gac gat cta gag acc aca gag gga tct ctc aag        768
```

11

Glu Asn Ala Trp Asp Asp Asp Leu Glu Thr Thr Glu Gly Ser Leu Lys
                    245   250   255

aaa ata att ggt aga aat gct agg att cag aca gag gca aag aag aaa   816
Lys Ile Ile Gly Arg Asn Ala Arg Ile Gln Thr Glu Ala Lys Lys Lys
                260   265   270

cta agc caa gat ctg ggt gtc tct ggt gaa att gga gac agt gta ggt   864
Leu Ser Gln Asp Leu Gly Val Ser Gly Glu Ile Gly Asp Ser Val Gly
                275   280   285

aat tgg cgg gaa agg ctt gca acc tgg aag gaa atg tta gaa cga gaa   912
Asn Trp Arg Glu Arg Leu Ala Thr Trp Lys Glu Met Leu Glu Arg Glu
        290   295   300

aaa tta tca gaa cag tta aac tcc tca gcg gcg aag tat gtg gtt gaa   960
Lys Leu Ser Glu Gln Leu Asn Ser Ser Ala Ala Lys Tyr Val Val Glu
305   310   315   320

ttt gat atg aaa gag gta gag aaa agt ctt cgc gaa gat gtt att gga   1008
Phe Asp Met Lys Glu Val Glu Lys Ser Leu Arg Glu Asp Val Ile Gly
                325   330   335

agg aca tct gaa act gag gga act aga gct ctc tgg ata tca aag aga   1056
Arg Thr Ser Glu Thr Glu Gly Thr Arg Ala Leu Trp Ile Ser Lys Arg
                340   345   350

tgg tgg cga tat cgc cct aag ctt ccc tat acc tac ttc ctt cag aag   1104
Trp Trp Arg Tyr Arg Pro Lys Leu Pro Tyr Thr Tyr Phe Leu Gln Lys
                355   360   365

ctt gat tct tct gag gtt gca gct gtt gtt ttc acg gaa gac cta aag   1152
Leu Asp Ser Ser Glu Val Ala Ala Val Val Phe Thr Glu Asp Leu Lys
        370   375   380

aga ttg tat gtg acc atg aaa gaa ggt ttc cct cta gaa tat att gtt   1200
Arg Leu Tyr Val Thr Met Lys Glu Gly Phe Pro Leu Glu Tyr Ile Val
385   390   395   400

gac att ccc tta gat cct tac ttg ttt gag act att tgc aac gcc gga   1248
Asp Ile Pro Leu Asp Pro Tyr Leu Phe Glu Thr Ile Cys Asn Ala Gly
                405   410   415

gtt gag gtg gat ctt ctt cag aag agg cag atc cac tac ttc atg aaa   1296
Val Glu Val Asp Leu Leu Gln Lys Arg Gln Ile His Tyr Phe Met Lys
                420   425   430

gtt ttc att gca ctt ctg ccg ggg ata cta att tta tgg ttt ata aga   1344
Val Phe Ile Ala Leu Leu Pro Gly Ile Leu Ile Leu Trp Phe Ile Arg
                435   440   445

gaa tct gcc atg ctt ctc ctt atc aca tcc aag cgc ttt ctc tac aag   1392
Glu Ser Ala Met Leu Leu Leu Ile Thr Ser Lys Arg Phe Leu Tyr Lys
        450   455   460

aag tat aat cag ctg ttt gat atg gct tat gca gaa aat ttt ata ttg   1440
Lys Tyr Asn Gln Leu Phe Asp Met Ala Tyr Ala Glu Asn Phe Ile Leu
465   470   475   480

ccg gtt gga gat gtc agt gag aca aaa tca atg tat aag gaa gtg gta   1488

12

```
Pro Val Gly Asp Val Ser Glu Thr Lys Ser Met Tyr Lys Glu Val Val
            485                 490                 495

cta ggc ggt gat gtc tgg gat ctt ctt gat gag cta atg atc tac atg    1536
Leu Gly Gly Asp Val Trp Asp Leu Leu Asp Glu Leu Met Ile Tyr Met
            500                 505                 510

ggg aac cca atg caa tac tat gaa aaa gat gtg gct ttt gtc agg ggt    1584
Gly Asn Pro Met Gln Tyr Tyr Glu Lys Asp Val Ala Phe Val Arg Gly
            515                 520                 525

gtg ctt ctt tct gga cct cct gga act gga aaa aca ctt ttt gcg cga    1632
Val Leu Leu Ser Gly Pro Pro Gly Thr Gly Lys Thr Leu Phe Ala Arg
        530                 535                 540

aca ctt gca aag gaa agt ggg cta cca ttt gtg ttt gca tct ggt gcg    1680
Thr Leu Ala Lys Glu Ser Gly Leu Pro Phe Val Phe Ala Ser Gly Ala
545                 550                 555                 560

gag ttc aca gac agt gaa aaa agt ggt gct gca aag atc aat gag atg    1728
Glu Phe Thr Asp Ser Glu Lys Ser Gly Ala Ala Lys Ile Asn Glu Met
                565                 570                 575

ttt tca atc gcg aga cga aat gcc cct gct ttt gtg ttt gtg gat gaa    1776
Phe Ser Ile Ala Arg Arg Asn Ala Pro Ala Phe Val Phe Val Asp Glu
            580                 585                 590

ata gat gct att gct ggt aga cat gct aga aaa gat cca cgg aga aga    1824
Ile Asp Ala Ile Ala Gly Arg His Ala Arg Lys Asp Pro Arg Arg Arg
            595                 600                 605

gca act ttt gaa gct tta att gcg caa ctc gat ggg gag aaa gag aag    1872
Ala Thr Phe Glu Ala Leu Ile Ala Gln Leu Asp Gly Glu Lys Glu Lys
        610                 615                 620

aca ggt atc gat agg ttt tct ttg aga caa gct gtg ata ttt atc tgt    1920
Thr Gly Ile Asp Arg Phe Ser Leu Arg Gln Ala Val Ile Phe Ile Cys
625                 630                 635                 640

gct acc aat aga cct gat gaa ctc gac ctt gag ttt gtc cgt tct ggc    1968
Ala Thr Asn Arg Pro Asp Glu Leu Asp Leu Glu Phe Val Arg Ser Gly
                645                 650                 655

cgt att gac cgt cgg ctg tat att ggg ttg cct gat gca aag caa agg    2016
Arg Ile Asp Arg Arg Leu Tyr Ile Gly Leu Pro Asp Ala Lys Gln Arg
            660                 665                 670

gtg caa ata ttt gga gtt cac agt gct ggg aag aac ctt gca gaa gat    2064
Val Gln Ile Phe Gly Val His Ser Ala Gly Lys Asn Leu Ala Glu Asp
            675                 680                 685

ata gac ttt ggg aag ctt gtt ttt cga acg gtt ggc ttt tcc ggg gca    2112
Ile Asp Phe Gly Lys Leu Val Phe Arg Thr Val Gly Phe Ser Gly Ala
            690                 695                 700

gat atc cgg aat ctt gtt aac gaa gcg gct ata atg tcg gta agg aag    2160
Asp Ile Arg Asn Leu Val Asn Glu Ala Ala Ile Met Ser Val Arg Lys
705                 710                 715                 720

gga cgt tct tac ata tat caa caa gac att gtt gat gtg tta gat aaa    2208
```

13

```
Gly Arg Ser Tyr Ile Tyr Gln Gln Asp Ile Val Asp Val Leu Asp Lys
                725             730             735


caa ttg ctc gag ggt atg ggt gta ctt ctt aca gag gaa gag caa cag       2256
Gln Leu Leu Glu Gly Met Gly Val Leu Leu Thr Glu Glu Glu Gln Gln
                740             745             750


aaa tgt gaa caa agt gta tct tac gaa aag aag aga ctt ctg gct gtt       2304
Lys Cys Glu Gln Ser Val Ser Tyr Glu Lys Lys Arg Leu Leu Ala Val
                755             760             765


cat gag gct ggt cat ata gtg ttg gct cat ttg ttt cct cga ttt gac       2352
His Glu Ala Gly His Ile Val Leu Ala His Leu Phe Pro Arg Phe Asp
        770             775             780


tgg cat gca ttt tcg cag ctc ctt cct ggt ggc aag gaa act gct gta       2400
Trp His Ala Phe Ser Gln Leu Leu Pro Gly Gly Lys Glu Thr Ala Val
785             790             795             800


tcg gtt ttc tat cca cgt gaa gac atg gta gac caa ggg tat acc acg       2448
Ser Val Phe Tyr Pro Arg Glu Asp Met Val Asp Gln Gly Tyr Thr Thr
                805             810             815


ttt ggt tat atg aaa atg caa atg gtg gta gct cat ggt gga cgc tgt       2496
Phe Gly Tyr Met Lys Met Gln Met Val Val Ala His Gly Gly Arg Cys
                820             825             830


gct gaa cgt gtg gtt ttt ggc gat aat gtc act gat gga gga aaa gat       2544
Ala Glu Arg Val Val Phe Gly Asp Asn Val Thr Asp Gly Gly Lys Asp
                835             840             845


gac ctg gag aag ata aca aaa att gcc agg gag atg gtg att agc cct       2592
Asp Leu Glu Lys Ile Thr Lys Ile Ala Arg Glu Met Val Ile Ser Pro
        850             855             860


caa agt gcg aga tta ggt ctc act caa ctt gta aaa aag att gga atg       2640
Gln Ser Ala Arg Leu Gly Leu Thr Gln Leu Val Lys Lys Ile Gly Met
865             870             875             880


gtg gat tta cca gat aac cca gac ggc gag ctg ata aaa tac cgg tgg       2688
Val Asp Leu Pro Asp Asn Pro Asp Gly Glu Leu Ile Lys Tyr Arg Trp
                885             890             895


gac cat cct cat gta atg cca gca gag atg tcg gta gaa gta tcc gag       2736
Asp His Pro His Val Met Pro Ala Glu Met Ser Val Glu Val Ser Glu
        900             905             910


cta ttc acc cgt gag ttg aca agg tat atc gag gag act gaa gaa ctt       2784
Leu Phe Thr Arg Glu Leu Thr Arg Tyr Ile Glu Glu Thr Glu Glu Leu
        915             920             925


gcg atg aat gct ctg aga gca aac agg cac att ctg gac tta atc acc       2832
Ala Met Asn Ala Leu Arg Ala Asn Arg His Ile Leu Asp Leu Ile Thr
        930             935             940


aga gag tta tta gaa aaa tca agg att act gga ttg gaa gtg gaa gag       2880
Arg Glu Leu Leu Glu Lys Ser Arg Ile Thr Gly Leu Glu Val Glu Glu
945             950             955             960


aaa atg aag gat ctt tct ccg tta atg ttt gag gat ttt gtg aag cca       2928
```

14

```
Lys Met Lys Asp Leu Ser Pro Leu Met Phe Glu Asp Phe Val Lys Pro
              965             970             975

ttc cag ata aac cct gat gat gag gag ctt tta cct cac aag gat cga    2976
Phe Gln Ile Asn Pro Asp Asp Glu Glu Leu Leu Pro His Lys Asp Arg
              980             985             990

gtg agc tat cag cca gtt gat tta cgt gct gcg cca ctc cac aga agc    3024
Val Ser Tyr Gln Pro Val Asp Leu Arg Ala Ala Pro Leu His Arg Ser
              995            1000            1005

tag                                                                3027
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<213> Arabidopsis thaliana

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Met Glu Ile Ala Ile Ser Tyr Lys Pro Asn Pro Leu Ile Ser Ser Ser
1               5               10              15


Thr Gln Leu Leu Lys Arg Ser Lys Ser Phe Gly Leu Val Arg Phe Pro
              20              25              30


Ala Lys Tyr Gly Leu Gly Ala Thr Arg Lys Lys Gln Leu Phe Arg Val
              35              40              45


Tyr Ala Ser Glu Ser Ser Ser Gly Ser Ser Ser Asn Ser Asp Gly Gly
       50              55              60


Phe Ser Trp Val Arg Leu Ala Gln Ser Ile Arg Leu Gly Ala Glu Arg
65              70              75              80


Ile Gly Glu Lys Ile Gly Glu Ser Val Lys Thr Glu Ile Gly Phe Asp
                 85              90              95


Ser Glu Glu Ala Ser Gly Arg Val Asn Glu Tyr Val Ala Arg Val Lys
              100             105             110


Asp Ser Val His Lys Gly His His Glu Leu Thr Arg Phe Lys Asn Glu
              115             120             125


Thr Val Pro Ser Phe Ile Asp Trp Asn Lys Trp Glu His Trp Lys Asp
              130             135             140
```

15

```
Ile Arg Asn Trp Asp Gly Lys Arg Val Ala Ala Leu Phe Ile Tyr Ala
145             150             155                 160

Phe Ala Leu Leu Leu Ser Cys Gln Arg Val Tyr Val Ala Ile Gln Ala
                165             170             175

Pro Arg Val Glu Arg Glu Arg Arg Glu Leu Thr Glu Ser Phe Met Glu
            180             185             190

Ala Leu Ile Pro Glu Pro Ser Pro Gly Asn Ile Glu Lys Phe Lys Arg
            195             200             205

Asn Met Trp Arg Lys Ala Thr Pro Lys Gly Leu Lys Leu Lys Arg Phe
        210             215             220

Ile Glu Ala Pro Asp Gly Thr Leu Val His Asp Ser Ser Tyr Val Gly
225             230             235                 240

Glu Asn Ala Trp Asp Asp Asp Leu Glu Thr Thr Glu Gly Ser Leu Lys
                245             250             255

Lys Ile Ile Gly Arg Asn Ala Arg Ile Gln Thr Glu Ala Lys Lys Lys
            260             265             270

Leu Ser Gln Asp Leu Gly Val Ser Gly Glu Ile Gly Asp Ser Val Gly
            275             280             285

Asn Trp Arg Glu Arg Leu Ala Thr Trp Lys Glu Met Leu Glu Arg Glu
        290             295             300

Lys Leu Ser Glu Gln Leu Asn Ser Ser Ala Ala Lys Tyr Val Val Glu
305             310             315                 320

Phe Asp Met Lys Glu Val Glu Lys Ser Leu Arg Glu Asp Val Ile Gly
                325             330             335

Arg Thr Ser Glu Thr Glu Gly Thr Arg Ala Leu Trp Ile Ser Lys Arg
            340             345             350

Trp Trp Arg Tyr Arg Pro Lys Leu Pro Tyr Thr Tyr Phe Leu Gln Lys
        355             360             365

Leu Asp Ser Ser Glu Val Ala Ala Val Val Phe Thr Glu Asp Leu Lys
        370             375             380
```

16

Arg Leu Tyr Val Thr Met Lys Glu Gly Phe Pro Leu Glu Tyr Ile Val
385   390   395   400

Asp Ile Pro Leu Asp Pro Tyr Leu Phe Glu Thr Ile Cys Asn Ala Gly
            405   410   415

Val Glu Val Asp Leu Leu Gln Lys Arg Gln Ile His Tyr Phe Met Lys
            420   425   430

Val Phe Ile Ala Leu Leu Pro Gly Ile Leu Ile Leu Trp Phe Ile Arg
        435   440   445

Glu Ser Ala Met Leu Leu Leu Ile Thr Ser Lys Arg Phe Leu Tyr Lys
        450   455   460

Lys Tyr Asn Gln Leu Phe Asp Met Ala Tyr Ala Glu Asn Phe Ile Leu
465   470   475   480

Pro Val Gly Asp Val Ser Glu Thr Lys Ser Met Tyr Lys Glu Val Val
            485   490   495

Leu Gly Gly Asp Val Trp Asp Leu Leu Asp Glu Leu Met Ile Tyr Met
            500   505   510

Gly Asn Pro Met Gln Tyr Tyr Glu Lys Asp Val Ala Phe Val Arg Gly
        515   520   525

Val Leu Leu Ser Gly Pro Pro Gly Thr Gly Lys Thr Leu Phe Ala Arg
    530   535   540

Thr Leu Ala Lys Glu Ser Gly Leu Pro Phe Val Phe Ala Ser Gly Ala
545   550   555   560

Glu Phe Thr Asp Ser Glu Lys Ser Gly Ala Ala Lys Ile Asn Glu Met
            565   570   575

Phe Ser Ile Ala Arg Arg Asn Ala Pro Ala Phe Val Phe Val Asp Glu
        580   585   590

Ile Asp Ala Ile Ala Gly Arg His Ala Arg Lys Asp Pro Arg Arg Arg
        595   600   605

Ala Thr Phe Glu Ala Leu Ile Ala Gln Leu Asp Gly Glu Lys Glu Lys
    610   615   620

17

Thr Gly Ile Asp Arg Phe Ser Leu Arg Gln Ala Val Ile Phe Ile Cys
625   630   635   640

Ala Thr Asn Arg Pro Asp Glu Leu Asp Leu Glu Phe Val Arg Ser Gly
                645   650   655

Arg Ile Asp Arg Arg Leu Tyr Ile Gly Leu Pro Asp Ala Lys Gln Arg
            660   665   670

Val Gln Ile Phe Gly Val His Ser Ala Gly Lys Asn Leu Ala Glu Asp
        675   680   685

Ile Asp Phe Gly Lys Leu Val Phe Arg Thr Val Gly Phe Ser Gly Ala
    690   695   700

Asp Ile Arg Asn Leu Val Asn Glu Ala Ala Ile Met Ser Val Arg Lys
705   710   715   720

Gly Arg Ser Tyr Ile Tyr Gln Gln Asp Ile Val Asp Val Leu Asp Lys
            725   730   735

Gln Leu Leu Glu Gly Met Gly Val Leu Leu Thr Glu Glu Glu Gln Gln
            740   745   750

Lys Cys Glu Gln Ser Val Ser Tyr Glu Lys Lys Arg Leu Leu Ala Val
        755   760   765

His Glu Ala Gly His Ile Val Leu Ala His Leu Phe Pro Arg Phe Asp
    770   775   780

Trp His Ala Phe Ser Gln Leu Leu Pro Gly Gly Lys Glu Thr Ala Val
785   790   795   800

Ser Val Phe Tyr Pro Arg Glu Asp Met Val Asp Gln Gly Tyr Thr Thr
                805   810   815

Phe Gly Tyr Met Lys Met Gln Met Val Val Ala His Gly Gly Arg Cys
            820   825   830

Ala Glu Arg Val Val Phe Gly Asp Asn Val Thr Asp Gly Gly Lys Asp
        835   840   845

Asp Leu Glu Lys Ile Thr Lys Ile Ala Arg Glu Met Val Ile Ser Pro
850   855   860

18

```
Gln Ser Ala Arg Leu Gly Leu Thr Gln Leu Val Lys Lys Ile Gly Met
865           ·         870           875           880


Val Asp Leu Pro Asp Asn Pro Asp Gly Glu Leu Ile Lys Tyr Arg Trp
                885           890               895


Asp His Pro His Val Met Pro Ala Glu Met Ser Val Glu Val Ser Glu
            900               905               910


Leu Phe Thr Arg Glu Leu Thr Arg Tyr Ile Glu Glu Thr Glu Glu Leu
        915               920           925


Ala Met Asn Ala Leu Arg Ala Asn Arg His Ile Leu Asp Leu Ile Thr
        930               935           940


Arg Glu Leu Leu Glu Lys Ser Arg Ile Thr Gly Leu Glu Val Glu Glu
945               950           955               960


Lys Met Lys Asp Leu Ser Pro Leu Met Phe Glu Asp Phe Val Lys Pro
                965               970           975


Phe Gln Ile Asn Pro Asp Asp Glu Glu Leu Leu Pro His Lys Asp Arg
                980               985           990


Val Ser Tyr Gln Pro Val Asp Leu   Arg Ala Ala Pro Leu   His Arg Ser
        995               1000           1005
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<211> 2550

<212> DNA

<213> Arabidopsis thaliana

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<223> 4563

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Met Thr Lys Ser Asn Gly His Asn Ala Thr Met Ile Val Thr Gly Ala
1             5                   10              15

tgc gac ttc tct tca tca ttc tcc ctc gcc tct tcc tcc tcc tcc acc      96
Cys Asp Phe Ser Ser Ser Phe Ser Leu Ala Ser Ser Ser Ser Ser Thr
            20                  25                  30

gtc tcc gtc aca acc ttc aac att tcc tct ctt tcc tct aac ccc aac     144
Val Ser Val Thr Thr Phe Asn Ile Ser Ser Leu Ser Ser Asn Pro Asn
            35                  40                  45

atc atc aat tcc agc tca act ctc ttc cgt tcc ctt tcc ttc tcc ctt     192
Ile Ile Asn Ser Ser Ser Thr Leu Phe Arg Ser Leu Ser Phe Ser Leu
        50                  55                  60

atc cgc cac cgc agc agc tac tca cgt cgc tct ctc cgc cgt ctc tct     240
Ile Arg His Arg Ser Ser Tyr Ser Arg Arg Ser Leu Arg Arg Leu Ser
65                  70                  75                  80

atc cac aca gtt cat gga aac aaa acc caa ttc ttc tct cac tcg tct     288
Ile His Thr Val His Gly Asn Lys Thr Gln Phe Phe Ser His Ser Ser
                85                  90                  95

aca cga act cca cca ctt ttc acg gct aat tcc aca gcc caa cga agc     336
Thr Arg Thr Pro Pro Leu Phe Thr Ala Asn Ser Thr Ala Gln Arg Ser
            100                 105                 110

ggg act ttc gtc gaa cac ctt aca ggc att aca gaa tcg gaa gaa gga     384
Gly Thr Phe Val Glu His Leu Thr Gly Ile Thr Glu Ser Glu Glu Gly
            115                 120                 125

atc agc gaa gcc aac ggt ttc ggt gat gta gag tct gct agg aac gac     432
Ile Ser Glu Ala Asn Gly Phe Gly Asp Val Glu Ser Ala Arg Asn Asp
        130                 135                 140

ata aga aac gtc gcg act cgt aga ata gag acg gag ttt gaa gtt aga     480
Ile Arg Asn Val Ala Thr Arg Arg Ile Glu Thr Glu Phe Glu Val Arg
145                 150                 155                 160

gaa ttg gaa gag ttg cct gag gaa tgg cga cgc tcg aag cta gct tgg     528
Glu Leu Glu Glu Leu Pro Glu Glu Trp Arg Arg Ser Lys Leu Ala Trp
                165                 170                 175

ctg tgt aaa gag gtt cca acg cat aag gcc gtg acg ctt gtg aga ctc     576
Leu Cys Lys Glu Val Pro Thr His Lys Ala Val Thr Leu Val Arg Leu
            180                 185                 190

ttg aat gct cag aag aaa tgg gtt cgt caa gag gac gct act tac atc     624
Leu Asn Ala Gln Lys Lys Trp Val Arg Gln Glu Asp Ala Thr Tyr Ile
            195                 200                 205

tct gtt cat tgt atg cga att cgt gag aac gaa act gga ttc agg gtg     672
Ser Val His Cys Met Arg Ile Arg Glu Asn Glu Thr Gly Phe Arg Val
        210                 215                 220

tat aga tgg atg aca caa cag aat tgg tac cgg ttt gat ttc ggg tta     720
Tyr Arg Trp Met Thr Gln Gln Asn Trp Tyr Arg Phe Asp Phe Gly Leu
225                 230                 235                 240

acg acg aag cta gct gaa tac ttg ggg aaa gaa cgg aaa ttt acg aaa     768
```

20

Thr Thr Lys Leu Ala Glu Tyr Leu Gly Lys Glu Arg Lys Phe Thr Lys
　　　　　　245　　　　　　　　　250　　　　　　　255

tgt cga gag gta ttt gat gat gtt ttg aat caa gga cgt gta cca agt　　816
Cys Arg Glu Val Phe Asp Asp Val Leu Asn Gln Gly Arg Val Pro Ser
　　　　　260　　　　　　　　265　　　　　　　270

gaa tct aca ttt cat att ctt gta gtt gcg tat cta agt agc tta tca　　864
Glu Ser Thr Phe His Ile Leu Val Val Ala Tyr Leu Ser Ser Leu Ser
　　　　275　　　　　　　　280　　　　　　　285

gta gaa ggt tgt ctc gag gaa gcg tgt agt gtt tac aat aga atg att　　912
Val Glu Gly Cys Leu Glu Glu Ala Cys Ser Val Tyr Asn Arg Met Ile
　　　290　　　　　　　　295　　　　　　　300

caa ctt gga ggt tac aaa ccg cgt ctt agt ctg cat aac tct ttg ttt　　960
Gln Leu Gly Gly Tyr Lys Pro Arg Leu Ser Leu His Asn Ser Leu Phe
305　　　　　　　　310　　　　　　　315　　　　　　　320

aga gct ttg gtt agt aaa caa gga ggg att ctg aat gat cag ctt aag　　1008
Arg Ala Leu Val Ser Lys Gln Gly Gly Ile Leu Asn Asp Gln Leu Lys
　　　　　　325　　　　　　　330　　　　　　　335

caa gca gag ttt atc ttt cac aat gtt gtg aca acc ggg ctt gag gtt　　1056
Gln Ala Glu Phe Ile Phe His Asn Val Val Thr Thr Gly Leu Glu Val
　　　　　340　　　　　　　345　　　　　　　350

cag aag gat att tat agt gga ttg atc tgg ctg cat agt tgt caa gat　　1104
Gln Lys Asp Ile Tyr Ser Gly Leu Ile Trp Leu His Ser Cys Gln Asp
　　　　355　　　　　　　360　　　　　　　365

gaa gtt gat ata ggt agg ata aac tct cta aga gaa gag atg aag aag　　1152
Glu Val Asp Ile Gly Arg Ile Asn Ser Leu Arg Glu Glu Met Lys Lys
　　　370　　　　　　　375　　　　　　　380

gcc ggt ttt cag gag agt aaa gaa gtt gtg gta tcg tta ctt aga gct　　1200
Ala Gly Phe Gln Glu Ser Lys Glu Val Val Val Ser Leu Leu Arg Ala
385　　　　　　　390　　　　　　　395　　　　　　　400

tat gca aag gag gga ggt gtg gaa gaa gtt gag agg acg tgg ctt gaa　　1248
Tyr Ala Lys Glu Gly Gly Val Glu Glu Val Glu Arg Thr Trp Leu Glu
　　　　　　405　　　　　　　410　　　　　　　415

ttg ctt gat tta gat tgt ggt ata cct tct cag gcg ttt gtg tac aaa　　1296
Leu Leu Asp Leu Asp Cys Gly Ile Pro Ser Gln Ala Phe Val Tyr Lys
　　　　　420　　　　　　　425　　　　　　　430

ata gaa gct tat tcg aaa gtc ggc gat ttt gcg aaa gct atg gag ata　　1344
Ile Glu Ala Tyr Ser Lys Val Gly Asp Phe Ala Lys Ala Met Glu Ile
　　　　435　　　　　　　440　　　　　　　445

ttt agg gag atg gag aag cat ata ggt ggt gca act atg tct gga tac　　1392
Phe Arg Glu Met Glu Lys His Ile Gly Gly Ala Thr Met Ser Gly Tyr
　　　450　　　　　　　455　　　　　　　460

cat aaa atc att gag gtt cta tgt aaa gtc caa caa gtg gaa ctt gtg　　1440
His Lys Ile Ile Glu Val Leu Cys Lys Val Gln Gln Val Glu Leu Val
465　　　　　　　470　　　　　　　475　　　　　　　480

gaa act ctc atg aag gag ttt gaa gaa agc ggg aag aag ccg ctt cta　　1488

21

```
Glu Thr Leu Met Lys Glu Phe Glu Glu Ser Gly Lys Lys Pro Leu Leu
              485                   490               495

cca tca ttc atc gaa ata gcc aaa atg tac ttc gat ttg ggt tta cat      1536
Pro Ser Phe Ile Glu Ile Ala Lys Met Tyr Phe Asp Leu Gly Leu His
              500                   505               510

gag aaa ttg gag atg gct ttt gtt cag tgc ttg gag aaa tgc caa cct      1584
Glu Lys Leu Glu Met Ala Phe Val Gln Cys Leu Glu Lys Cys Gln Pro
              515                   520               525

agc cag cct ata tat aac ata tat ttg gat tca ttg act aaa ata ggc      1632
Ser Gln Pro Ile Tyr Asn Ile Tyr Leu Asp Ser Leu Thr Lys Ile Gly
              530                   535               540

aac ctt gag aaa gca ggg gat gtc ttc aat gaa atg aaa aac aac ggg      1680
Asn Leu Glu Lys Ala Gly Asp Val Phe Asn Glu Met Lys Asn Asn Gly
545                   550                   555               560

aca atc aat gtg agt gct aga tcc tgc aac agc ctt tta aag gga tac      1728
Thr Ile Asn Val Ser Ala Arg Ser Cys Asn Ser Leu Leu Lys Gly Tyr
                  565                   570               575

cta gat tgt gga aaa caa gtg cag gca gag aga ata tat gat ctg atg      1776
Leu Asp Cys Gly Lys Gln Val Gln Ala Glu Arg Ile Tyr Asp Leu Met
                  580                   585               590

aga atg aag aaa tac gaa atc gaa cca ccg ctt atg gaa aag ctt gat      1824
Arg Met Lys Lys Tyr Glu Ile Glu Pro Pro Leu Met Glu Lys Leu Asp
              595                   600                   605

tac atc ctg agc ttg aag aaa aaa gag gtg aag aag aga ccg ttt agc      1872
Tyr Ile Leu Ser Leu Lys Lys Lys Glu Val Lys Lys Arg Pro Phe Ser
          610                   615                   620

atg aag cta agc aaa gac cag cgt gag gta ttg gta ggt ttg ttg tta      1920
Met Lys Leu Ser Lys Asp Gln Arg Glu Val Leu Val Gly Leu Leu Leu
625                   630                   635               640

ggt ggc ttg caa atc gaa tca gac aaa gag aag aag agc cac atg atc      1968
Gly Gly Leu Gln Ile Glu Ser Asp Lys Glu Lys Lys Ser His Met Ile
                  645                   650               655

aaa ttt gaa ttt aga gaa aat tct caa gct cat ctg gtt ctt aaa caa      2016
Lys Phe Glu Phe Arg Glu Asn Ser Gln Ala His Leu Val Leu Lys Gln
              660                   665               670

aac ata cat gac cag ttc cgt gag tgg ttg cat cct ttg agc aat ttt      2064
Asn Ile His Asp Gln Phe Arg Glu Trp Leu His Pro Leu Ser Asn Phe
          675                   680                   685

cag gag gat att ata ccg ttc gaa ttc tac tcc gtt ccc cat tca tac      2112
Gln Glu Asp Ile Ile Pro Phe Glu Phe Tyr Ser Val Pro His Ser Tyr
          690                   695                   700

ttc ggg ttt tac gct gaa cat tac tgg cca aag ggt cag cca gag att      2160
Phe Gly Phe Tyr Ala Glu His Tyr Trp Pro Lys Gly Gln Pro Glu Ile
705                   710                   715               720

cca aaa ctg att cat cgg tgg cta tcg cca cac tca ctc gcg tat tgg      2208
```

22

```
Pro Lys Leu Ile His Arg Trp Leu Ser Pro His Ser Leu Ala Tyr Trp
            725                 730                 735

tac atg tac agc ggc gtt aaa aca tca tca gga gac att atc ttg aga      2256
Tyr Met Tyr Ser Gly Val Lys Thr Ser Ser Gly Asp Ile Ile Leu Arg
            740                 745                 750

ttg aag gga agt ctc gaa ggt gtt gac aaa gta gta aag gct ctt caa      2304
Leu Lys Gly Ser Leu Glu Gly Val Glu Lys Val Val Lys Ala Leu Gln
            755                 760                 765

gcc aaa tct atg gaa tgt cga gtt aag aag aaa gga aaa gtc ttc tgg      2352
Ala Lys Ser Met Glu Cys Arg Val Lys Lys Lys Gly Lys Val Phe Trp
            770                 775                 780

att gga ctt cag gga aca aac tca gct ttg ttc tgg aaa cta ata gag      2400
Ile Gly Leu Gln Gly Thr Asn Ser Ala Leu Phe Trp Lys Leu Ile Glu
785                 790                 795                 800

cct cat gtg tta gag aac ttg aaa gag cat ttg aaa cct gct tct gaa      2448
Pro His Val Leu Glu Asn Leu Lys Glu His Leu Lys Pro Ala Ser Glu
                    805                 810                 815

tca ctg gac aat gtt aag gaa gca gaa gaa caa agc atc aac ttc aaa      2496
Ser Leu Asp Asn Val Lys Glu Ala Glu Glu Gln Ser Ile Asn Phe Lys
                820                 825                 830

tca aac tct gat cac agt gac gat tgt gtc aat tca gaa gca cat ttt      2544
Ser Asn Ser Asp His Ser Asp Asp Cys Val Asn Ser Glu Ala His Phe
                835                 840                 845

tac tga                                                              2550
Tyr
```

```
<210>   8

<211>   849

<212>   PRT

<213>   Arabidopsis thaliana


<400>   8

Met Thr Lys Ser Asn Gly His Asn Ala Thr Met Ile Val Thr Gly Ala
1               5                   10                  15


Cys Asp Phe Ser Ser Ser Phe Ser Leu Ala Ser Ser Ser Ser Ser Thr
                20                  25                  30


Val Ser Val Thr Thr Phe Asn Ile Ser Ser Leu Ser Ser Asn Pro Asn
            35                  40                  45
```

23

```
Ile Ile Asn Ser Ser Ser Thr Leu Phe Arg Ser Leu Ser Phe Ser Leu
    50              55              60

Ile Arg His Arg Ser Ser Tyr Ser Arg Arg Ser Leu Arg Arg Leu Ser
65              70              75              80

Ile His Thr Val His Gly Asn Lys Thr Gln Phe Phe Ser His Ser Ser
                85              90              95

Thr Arg Thr Pro Pro Leu Phe Thr Ala Asn Ser Thr Ala Gln Arg Ser
            100             105             110

Gly Thr Phe Val Glu His Leu Thr Gly Ile Thr Glu Ser Glu Glu Gly
        115             120             125

Ile Ser Glu Ala Asn Gly Phe Gly Asp Val Glu Ser Ala Arg Asn Asp
    130             135             140

Ile Arg Asn Val Ala Thr Arg Arg Ile Glu Thr Glu Phe Glu Val Arg
145             150             155             160

Glu Leu Glu Glu Leu Pro Glu Glu Trp Arg Arg Ser Lys Leu Ala Trp
            165             170             175

Leu Cys Lys Glu Val Pro Thr His Lys Ala Val Thr Leu Val Arg Leu
            180             185             190

Leu Asn Ala Gln Lys Lys Trp Val Arg Gln Glu Asp Ala Thr Tyr Ile
        195             200             205

Ser Val His Cys Met Arg Ile Arg Glu Asn Glu Thr Gly Phe Arg Val
    210             215             220

Tyr Arg Trp Met Thr Gln Gln Asn Trp Tyr Arg Phe Asp Phe Gly Leu
225             230             235             240

Thr Thr Lys Leu Ala Glu Tyr Leu Gly Lys Glu Arg Lys Phe Thr Lys
            245             250             255

Cys Arg Glu Val Phe Asp Asp Val Leu Asn Gln Gly Arg Val Pro Ser
            260             265             270

Glu Ser Thr Phe His Ile Leu Val Val Ala Tyr Leu Ser Ser Leu Ser
        275             280             285
```

24

Val Glu Gly Cys Leu Glu Glu Ala Cys Ser Val Tyr Asn Arg Met Ile
    290   295   300

Gln Leu Gly Gly Tyr Lys Pro Arg Leu Ser Leu His Asn Ser Leu Phe
305   310   315   320

Arg Ala Leu Val Ser Lys Gln Gly Gly Ile Leu Asn Asp Gln Leu Lys
                325   330   335

Gln Ala Glu Phe Ile Phe His Asn Val Val Thr Thr Gly Leu Glu Val
            340   345   350

Gln Lys Asp Ile Tyr Ser Gly Leu Ile Trp Leu His Ser Cys Gln Asp
        355   360   365

Glu Val Asp Ile Gly Arg Ile Asn Ser Leu Arg Glu Glu Met Lys Lys
    370   375   380

Ala Gly Phe Gln Glu Ser Lys Glu Val Val Val Ser Leu Leu Arg Ala
385   390   395   400

Tyr Ala Lys Glu Gly Gly Val Glu Glu Val Glu Arg Thr Trp Leu Glu
            405   410   415

Leu Leu Asp Leu Asp Cys Gly Ile Pro Ser Gln Ala Phe Val Tyr Lys
        420   425   430

Ile Glu Ala Tyr Ser Lys Val Gly Asp Phe Ala Lys Ala Met Glu Ile
    435   440   445

Phe Arg Glu Met Glu Lys His Ile Gly Gly Ala Thr Met Ser Gly Tyr
450   455   460

His Lys Ile Ile Glu Val Leu Cys Lys Val Gln Gln Val Glu Leu Val
465   470   475   480

Glu Thr Leu Met Lys Glu Phe Glu Glu Ser Gly Lys Lys Pro Leu Leu
            485   490   495

Pro Ser Phe Ile Glu Ile Ala Lys Met Tyr Phe Asp Leu Gly Leu His
            500   505   510

Glu Lys Leu Glu Met Ala Phe Val Gln Cys Leu Glu Lys Cys Gln Pro
        515   520   525

25

```
Ser Gln Pro Ile Tyr Asn Ile Tyr Leu Asp Ser Leu Thr Lys Ile Gly
    530             535             540

Asn Leu Glu Lys Ala Gly Asp Val Phe Asn Glu Met Lys Asn Asn Gly
545             550             555             560

Thr Ile Asn Val Ser Ala Arg Ser Cys Asn Ser Leu Leu Lys Gly Tyr
                565             570             575

Leu Asp Cys Gly Lys Gln Val Gln Ala Glu Arg Ile Tyr Asp Leu Met
            580             585             590

Arg Met Lys Lys Tyr Glu Ile Glu Pro Pro Leu Met Glu Lys Leu Asp
            595             600             605

Tyr Ile Leu Ser Leu Lys Lys Lys Glu Val Lys Lys Arg Pro Phe Ser
    610             615             620

Met Lys Leu Ser Lys Asp Gln Arg Glu Val Leu Val Gly Leu Leu Leu
625             630             635             640

Gly Gly Leu Gln Ile Glu Ser Asp Lys Glu Lys Lys Ser His Met Ile
                645             650             655

Lys Phe Glu Phe Arg Glu Asn Ser Gln Ala His Leu Val Leu Lys Gln
            660             665             670

Asn Ile His Asp Gln Phe Arg Glu Trp Leu His Pro Leu Ser Asn Phe
            675             680             685

Gln Glu Asp Ile Ile Pro Phe Glu Phe Tyr Ser Val Pro His Ser Tyr
    690             695             700

Phe Gly Phe Tyr Ala Glu His Tyr Trp Pro Lys Gly Gln Pro Glu Ile
705             710             715             720

Pro Lys Leu Ile His Arg Trp Leu Ser Pro His Ser Leu Ala Tyr Trp
                725             730             735

Tyr Met Tyr Ser Gly Val Lys Thr Ser Ser Gly Asp Ile Ile Leu Arg
            740             745             750

Leu Lys Gly Ser Leu Glu Gly Val Glu Lys Val Val Lys Ala Leu Gln
            755             760             765
```

26

```
Ala Lys Ser Met Glu Cys Arg Val Lys Lys Lys Gly Lys Val Phe Trp
    770                 775             780
```

```
Ile Gly Leu Gln Gly Thr Asn Ser Ala Leu Phe Trp Lys Leu Ile Glu
785                 790             795             800
```

```
Pro His Val Leu Glu Asn Leu Lys Glu His Leu Lys Pro Ala Ser Glu
                805             810             815
```

```
Ser Leu Asp Asn Val Lys Glu Ala Glu Glu Gln Ser Ile Asn Phe Lys
            820             825             830
```

```
Ser Asn Ser Asp His Ser Asp Asp Cys Val Asn Ser Glu Ala His Phe
        835             840             845
```

```
Tyr
```

<210> 9

<211> 1449

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1449)

<223> 8794

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<400> 9
atg gtt gga tct ttg gaa tct gat caa act ctt tca atg gcc acc tta      48
Met Val Gly Ser Leu Glu Ser Asp Gln Thr Leu Ser Met Ala Thr Leu
1               5               10              15
```

```
atc gaa aaa ctc gac atc tta tct gac gac ttc gat cca acc gcc gta      96
Ile Glu Lys Leu Asp Ile Leu Ser Asp Asp Phe Asp Pro Thr Ala Val
            20              25              30
```

```
gtc acc gaa ccg tta cct cct ccg gta act aat gga atc gga gct gat     144
Val Thr Glu Pro Leu Pro Pro Pro Val Thr Asn Gly Ile Gly Ala Asp
        35              40              45
```

```
aaa gga gga gga gga gga gaa aga gag atg gtt ctc ggt agg aat ata     192
Lys Gly Gly Gly Gly Gly Glu Arg Glu Met Val Leu Gly Arg Asn Ile
    50              55              60
```

27

```
cac aca acg tca ctc gct gta acg gaa ccg gag gtt aac gat gaa ttc     240
His Thr Thr Ser Leu Ala Val Thr Glu Pro Glu Val Asn Asp Glu Phe
65                  70                  75                  80

acc gga gat aaa gaa gct tat atg gct agt gtt ctt gct cgt tac cgg     288
Thr Gly Asp Lys Glu Ala Tyr Met Ala Ser Val Leu Ala Arg Tyr Arg
                    85                  90                  95

aaa act ttg gtt gaa cga acc aaa aac cat tta ggt tat cct tat aac     336
Lys Thr Leu Val Glu Arg Thr Lys Asn His Leu Gly Tyr Pro Tyr Asn
                100                 105                 110

ttg gat ttc gac tat ggt gcg ctt ggt cag tta caa cat ttt tcg att    384
Leu Asp Phe Asp Tyr Gly Ala Leu Gly Gln Leu Gln His Phe Ser Ile
            115                 120                 125

aat aat ctt gga gat ccg ttt att gaa agt aac tat ggt gta cac tca    432
Asn Asn Leu Gly Asp Pro Phe Ile Glu Ser Asn Tyr Gly Val His Ser
        130                 135                 140

aga cct ttt gaa gtt ggt gtg ttg gat tgg ttt gct cgt ctt tgg gag   480
Arg Pro Phe Glu Val Gly Val Leu Asp Trp Phe Ala Arg Leu Trp Glu
145                 150                 155                 160

att gag aga gat gat tat tgg ggt tac att acc aat tgt ggt act gaa    528
Ile Glu Arg Asp Asp Tyr Trp Gly Tyr Ile Thr Asn Cys Gly Thr Glu
                    165                 170                 175

ggc aac ctt cat ggc att tta gtc ggg agg gag atg ttt ccg gat ggg    576
Gly Asn Leu His Gly Ile Leu Val Gly Arg Glu Met Phe Pro Asp Gly
                180                 185                 190

ata ttg tat gcg tcg cgt gaa tcg cat tac tcg gtg ttt aaa gct gct    624
Ile Leu Tyr Ala Ser Arg Glu Ser His Tyr Ser Val Phe Lys Ala Ala
            195                 200                 205

cga atg tat cga atg gag tgt gag aag gtt gat acg ctt atg tca ggg    672
Arg Met Tyr Arg Met Glu Cys Glu Lys Val Asp Thr Leu Met Ser Gly
        210                 215                 220

gag att gat tgt gat gat ttg agg aag aag ttg ttg gct aat aaa gat    720
Glu Ile Asp Cys Asp Asp Leu Arg Lys Lys Leu Leu Ala Asn Lys Asp
225                 230                 235                 240

aaa ccg gcg att ctt aat gtt aac ata gga acg acg gtt aaa gga gct    768
Lys Pro Ala Ile Leu Asn Val Asn Ile Gly Thr Thr Val Lys Gly Ala
                    245                 250                 255

gtt gat gat ctt gac ctt gtt atc aaa act ctt gaa gag tgt ggt ttc    816
Val Asp Asp Leu Asp Leu Val Ile Lys Thr Leu Glu Glu Cys Gly Phe
                260                 265                 270

tca cat gat agg ttc tat att cat tgt gat gga gct ttg ttt gga ctt    864
Ser His Asp Arg Phe Tyr Ile His Cys Asp Gly Ala Leu Phe Gly Leu
        275                 280                 285

atg atg cct ttt gtc aaa cgt gca ccg aaa gtg acg ttt aat aaa ccg    912
Met Met Pro Phe Val Lys Arg Ala Pro Lys Val Thr Phe Asn Lys Pro
290                 295                 300
```

28

```
ata ggg agt gtg agt gta tcg ggc cac aaa ttt gtc ggg tgt cca atg        960
Ile Gly Ser Val Ser Val Ser Gly His Lys Phe Val Gly Cys Pro Met
305                 310                 315                 320

cca tgt ggt gtt cag ata aca aga atg gaa cat atc aaa gtc ctc tcc       1008
Pro Cys Gly Val Gln Ile Thr Arg Met Glu His Ile Lys Val Leu Ser
                325                 330                 335

agt aac gtt gag tac ctt gct tca agg gat gca aca atc atg gga agt       1056
Ser Asn Val Glu Tyr Leu Ala Ser Arg Asp Ala Thr Ile Met Gly Ser
                340                 345                 350

cgt aac ggg cat gct cct ttg ttc ctc tgg tac acc tta aac agg aaa       1104
Arg Asn Gly His Ala Pro Leu Phe Leu Trp Tyr Thr Leu Asn Arg Lys
                355                 360                 365

ggt tac aaa gga ttc cag aaa gaa gtt cag aaa tgc ttg aga aac gcg       1152
Gly Tyr Lys Gly Phe Gln Lys Glu Val Gln Lys Cys Leu Arg Asn Ala
        370                 375                 380

cat tac ctc aaa gac cga ctt cgt gaa gct ggg att agc gcc atg ctt       1200
His Tyr Leu Lys Asp Arg Leu Arg Glu Ala Gly Ile Ser Ala Met Leu
385                 390                 395                 400

aat gag ctt agc agc act gtg gtc ttt gaa cgg cct aaa gat gaa gag       1248
Asn Glu Leu Ser Ser Thr Val Val Phe Glu Arg Pro Lys Asp Glu Glu
                405                 410                 415

ttt gtt aga agg tgg cag ctt gct tgc caa ggt gat ata gct cat gtg       1296
Phe Val Arg Arg Trp Gln Leu Ala Cys Gln Gly Asp Ile Ala His Val
        420                 425                 430

gtg gtt atg cca agt gtt aca atc gag aag ctt gat aat ttc ctg aaa       1344
Val Val Met Pro Ser Val Thr Ile Glu Lys Leu Asp Asn Phe Leu Lys
        435                 440                 445

gac ctt gtc aaa cac aga ttg atc tgg tac gag gat gga tct cag cct       1392
Asp Leu Val Lys His Arg Leu Ile Trp Tyr Glu Asp Gly Ser Gln Pro
        450                 455                 460

cct tgc ctt gca tcg gag gta gga acc aac aac tgc atc tgt cca gct       1440
Pro Cys Leu Ala Ser Glu Val Gly Thr Asn Asn Cys Ile Cys Pro Ala
465                 470                 475                 480

cac aag tga                                                           1449
His Lys
```

```
<210>  10

<211>  482

<212>  PRT

<213>  Arabidopsis thaliana
```

<400> 10

```
Met Val Gly Ser Leu Glu Ser Asp Gln Thr Leu Ser Met Ala Thr Leu
1               5                   10                  15

Ile Glu Lys Leu Asp Ile Leu Ser Asp Asp Phe Asp Pro Thr Ala Val
            20                  25                  30

Val Thr Glu Pro Leu Pro Pro Val Thr Asn Gly Ile Gly Ala Asp
            35                  40                  45

Lys Gly Gly Gly Gly Gly Glu Arg Glu Met Val Leu Gly Arg Asn Ile
        50                  55                  60

His Thr Thr Ser Leu Ala Val Thr Glu Pro Glu Val Asn Asp Glu Phe
65                  70                  75                  80

Thr Gly Asp Lys Glu Ala Tyr Met Ala Ser Val Leu Ala Arg Tyr Arg
                85                  90                  95

Lys Thr Leu Val Glu Arg Thr Lys Asn His Leu Gly Tyr Pro Tyr Asn
                100                 105                 110

Leu Asp Phe Asp Tyr Gly Ala Leu Gly Gln Leu Gln His Phe Ser Ile
            115                 120                 125

Asn Asn Leu Gly Asp Pro Phe Ile Glu Ser Asn Tyr Gly Val His Ser
        130                 135                 140

Arg Pro Phe Glu Val Gly Val Leu Asp Trp Phe Ala Arg Leu Trp Glu
145                 150                 155                 160

Ile Glu Arg Asp Asp Tyr Trp Gly Tyr Ile Thr Asn Cys Gly Thr Glu
                165                 170                 175

Gly Asn Leu His Gly Ile Leu Val Gly Arg Glu Met Phe Pro Asp Gly
            180                 185                 190

Ile Leu Tyr Ala Ser Arg Glu Ser His Tyr Ser Val Phe Lys Ala Ala
            195                 200                 205

Arg Met Tyr Arg Met Glu Cys Glu Lys Val Asp Thr Leu Met Ser Gly
        210                 215                 220

Glu Ile Asp Cys Asp Asp Leu Arg Lys Lys Leu Leu Ala Asn Lys Asp
        225                 230                 235                 240
```

30

```
Lys Pro Ala Ile Leu Asn Val Asn Ile Gly Thr Thr Val Lys Gly Ala
            245             250                 255

Val Asp Asp Leu Asp Leu Val Ile Lys Thr Leu Glu Glu Cys Gly Phe
            260             265                 270

Ser His Asp Arg Phe Tyr Ile His Cys Asp Gly Ala Leu Phe Gly Leu
            275             280                 285

Met Met Pro Phe Val Lys Arg Ala Pro Lys Val Thr Phe Asn Lys Pro
            290             295                 300

Ile Gly Ser Val Ser Val Ser Gly His Lys Phe Val Gly Cys Pro Met
305             310             315                 320

Pro Cys Gly Val Gln Ile Thr Arg Met Glu His Ile Lys Val Leu Ser
            325             330                 335

Ser Asn Val Glu Tyr Leu Ala Ser Arg Asp Ala Thr Ile Met Gly Ser
            340             345                 350

Arg Asn Gly His Ala Pro Leu Phe Leu Trp Tyr Thr Leu Asn Arg Lys
            355             360                 365

Gly Tyr Lys Gly Phe Gln Lys Glu Val Gln Lys Cys Leu Arg Asn Ala
370             375             380

His Tyr Leu Lys Asp Arg Leu Arg Glu Ala Gly Ile Ser Ala Met Leu
385             390             395                 400

Asn Glu Leu Ser Ser Thr Val Val Phe Glu Arg Pro Lys Asp Glu Glu
            405             410                 415

Phe Val Arg Arg Trp Gln Leu Ala Cys Gln Gly Asp Ile Ala His Val
            420             425                 430

Val Val Met Pro Ser Val Thr Ile Glu Lys Leu Asp Asn Phe Leu Lys
            435             440                 445

Asp Leu Val Lys His Arg Leu Ile Trp Tyr Glu Asp Gly Ser Gln Pro
450             455             460

Pro Cys Leu Ala Ser Glu Val Gly Thr Asn Asn Cys Ile Cys Pro Ala
465             470             475                 480
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31

His Lys

<210>   11

<211>   483

<212>   DNA

<213>   Arabidopsis thaliana

<220>

<221>   CDS

<222>   (1)..(483)

<223>   9106

<400>   11

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atg gcg gaa cag act gag aaa gct ttt ctt aag cag cct aag gtc ttc        48
Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val Phe
1               5                   10                  15

ctt agc tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga        96
Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly
                20                  25                  30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa       144
Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu
            35                  40                  45

gcc att gat gga gct tac gtt gac aag aaa tgc ccc ttc act gga act       192
Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly Thr
        50                  55                  60

gtt tcc att aga ggt cgt atc tta gct ggt act tgc cac agt gcg aaa       240
Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala Lys
65                  70                  75                  80

atg cag agg acc att atc gtg cga agg gat tac ctt cac ttt gtg aag       288
Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val Lys
                85                  90                  95

aag tat cag agg tat gag aag agg cat tca aac att ccg gct cat gtc       336
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Val
                100                 105                 110

tca cca tgc ttc cgt gtt aag gaa gga gac cat atc atc att ggc caa       384
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln
            115                 120                 125

tgc agg cca ttg tcg aag aca gtg agg ttc aat gtg ttg aag gtg ata       432
```

```
Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val Ile
    130             135             140

cca gct ggg tct tct tct tca ttt gga aag aag gca ttc act gga atg        480
Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly Met
145             150             155             160

taa                                                                    483
```

<210> 12

<211> 160

<212> PRT

<213> Arabidopsis thaliana

<400> 12

```
Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val Phe
1               5               10              15


Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly
            20              25              30


Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu
            35              40              45


Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly Thr
    50              55              60


Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala Lys
65              70              75              80


Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val Lys
                85              90              95


Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Val
            100             105             110


Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln
            115             120             125


Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val Ile
    130             135             140


Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly Met
145             150             155             160
```

```
<210>   13

<211>   1170

<212>   DNA

<213>   Arabidopsis thaliana


<220>

<221>   CDS

<222>   (1)..(1170)

<223>   10708


<400>   13
atg tct cac agg aag ttt gag cac cca aga cat ggt tct ctt ggt ttc        48
Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe
1               5                   10                  15

ctt cca agg aag aga gct aac cgt cac aga gga aag gtg aag gcg ttc        96
Leu Pro Arg Lys Arg Ala Asn Arg His Arg Gly Lys Val Lys Ala Phe
                20                  25                  30

cct aag gat gac caa acc aag cct tgc aag ttc aca gct ttc atg ggt       144
Pro Lys Asp Asp Gln Thr Lys Pro Cys Lys Phe Thr Ala Phe Met Gly
            35                  40                  45

tac aaa gct ggt atg act cac att gtc aga gaa gtg gag aaa cct gga       192
Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly
        50                  55                  60

tcc aag ctt cac aag aag gag aca tgt gag gct gtt acc atc att gag       240
Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu
65                  70                  75                  80

aca cct gct atg gtg gtt gtt gga gtt gtt gcc tat gtg aag act cct       288
Thr Pro Ala Met Val Val Val Gly Val Val Ala Tyr Val Lys Thr Pro
                85                  90                  95

aga ggt ttg agg tct ttg aac act gtc tgg gca cag cat ttg agt gag       336
Arg Gly Leu Arg Ser Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu
                100                 105                 110

gag gtc agg aga agg ttc tac aag aac tgg gct aag tct aag aag aag       384
Glu Val Arg Arg Arg Phe Tyr Lys Asn Trp Ala Lys Ser Lys Lys Lys
            115                 120                 125

gct ttc act ggg tac gct aag cag tat gac agt gag gat ggc aag aag       432
Ala Phe Thr Gly Tyr Ala Lys Gln Tyr Asp Ser Glu Asp Gly Lys Lys
        130                 135                 140

ggt att cag gct cag ctt gag aag atg aag aag tac gct act gtc atc       480
```

34

```
Gly Ile Gln Ala Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Ile
145             150             155             160

cgt gtt ttg gct cac act cag atc agg aag atg aag gga ttg aag cag     528
Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln
                165             170             175

aag aag gct cac atg atg gag atc cag atc aat ggt ggt acc att gcc     576
Lys Lys Ala His Met Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala
                180             185             190

cag aag gtt gac ttt gcc tac agt ttc ttt gag aag cag atc cca att     624
Gln Lys Val Asp Phe Ala Tyr Ser Phe Phe Glu Lys Gln Ile Pro Ile
                195             200             205

gaa gct gtc ttc cag aag gat gaa atg att gat atc att ggt gtg acc     672
Glu Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr
    210             215             220

aag ggt aag ggt tat gaa ggt gtt gtt act cgt tgg ggt gtt acc cgt     720
Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg
225             230             235             240

ctt cct cgt aag act cac aga ggt ctg cgt aag gtt gct tgt att ggt     768
Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly
                245             250             255

gcg tgg cat cct gct aga gtg tcc tac act gtt gct agg gct ggt cag     816
Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln
                260             265             270

aac ggt tac cat cac cgt act gag ctt aac aag aag att tac agg ttg     864
Asn Gly Tyr His His Arg Thr Glu Leu Asn Lys Lys Ile Tyr Arg Leu
                275             280             285

ggt aag gtt ggt act gag gca cac aca gcc atg act gaa tat gac agg     912
Gly Lys Val Gly Thr Glu Ala His Thr Ala Met Thr Glu Tyr Asp Arg
                290             295             300

act gag aag gat gtg act cca atg gga ggc ttc cca cac tac ggt att     960
Thr Glu Lys Asp Val Thr Pro Met Gly Gly Phe Pro His Tyr Gly Ile
305             310             315             320

gtg aag gat gac tac ttg atg att aag ggg tgc tgt gtt ggt ccc aag    1008
Val Lys Asp Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys
                325             330             335

aag aga gtt gta act ctc aga cag tca ctt ctc act cag act tcc cgt    1056
Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Thr Gln Thr Ser Arg
                340             345             350

ctt gcc ttg gag gag atc aaa ctc aag ttt att gac acc gcc tcc att    1104
Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ala Ser Ile
                355             360             365

ttt gga cat ggt cgc ttc cag acc tcc ctt gag aag atg agg ttt tac    1152
Phe Gly His Gly Arg Phe Gln Thr Ser Leu Glu Lys Met Arg Phe Tyr
                370             375             380

aac cgt gtc acg aag taa                                            1170
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Asn Arg Val Thr Lys
385


<210>  14

<211>  389

<212>  PRT

<213>  Arabidopsis thaliana


<400>  14

Met Ser His Arg Lys Phe Glu His Pro Arg His Gly Ser Leu Gly Phe
1               5                   10                  15


Leu Pro Arg Lys Arg Ala Asn Arg His Arg Gly Lys Val Lys Ala Phe
            20                  25                  30


Pro Lys Asp Asp Gln Thr Lys Pro Cys Lys Phe Thr Ala Phe Met Gly
            35                  40                  45


Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Glu Lys Pro Gly
    50                  55                  60


Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu
65                  70                  75                  80


Thr Pro Ala Met Val Val Val Gly Val Val Ala Tyr Val Lys Thr Pro
                85                  90                  95


Arg Gly Leu Arg Ser Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu
            100                 105                 110


Glu Val Arg Arg Arg Phe Tyr Lys Asn Trp Ala Lys Ser Lys Lys Lys
            115                 120                 125


Ala Phe Thr Gly Tyr Ala Lys Gln Tyr Asp Ser Glu Asp Gly Lys Lys
    130                 135                 140


Gly Ile Gln Ala Gln Leu Glu Lys Met Lys Lys Tyr Ala Thr Val Ile
145                 150                 155                 160


Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln
                165                 170                 175
```

```
Lys Lys Ala His Met Met Glu Ile Gln Ile Asn Gly Gly Thr Ile Ala
            180                 185             190

Gln Lys Val Asp Phe Ala Tyr Ser Phe Phe Glu Lys Gln Ile Pro Ile
            195                 200             205

Glu Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr
    210                 215             220

Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg
225                 230             235                 240

Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly
            245                 250             255

Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln
            260                 265             270

Asn Gly Tyr His His Arg Thr Glu Leu Asn Lys Lys Ile Tyr Arg Leu
            275                 280             285

Gly Lys Val Gly Thr Glu Ala His Thr Ala Met Thr Glu Tyr Asp Arg
    290                 295             300

Thr Glu Lys Asp Val Thr Pro Met Gly Gly Phe Pro His Tyr Gly Ile
305                 310             315                 320

Val Lys Asp Asp Tyr Leu Met Ile Lys Gly Cys Cys Val Gly Pro Lys
            325                 330             335

Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Thr Gln Thr Ser Arg
            340                 345             350

Leu Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ala Ser Ile
            355                 360             365

Phe Gly His Gly Arg Phe Gln Thr Ser Leu Glu Lys Met Arg Phe Tyr
            370                 375             380

Asn Arg Val Thr Lys
385


<210>   15

<211>   351
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<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(351)

<223> 10844

<400> 15

atg	aag	cca	gtg	ata	ggc	aca	gtg	gta	tcg	aac	aag	atg	caa	aaa	tct	48
Met	Lys	Pro	Val	Ile	Gly	Thr	Val	Val	Ser	Asn	Lys	Met	Gln	Lys	Ser	
1				5					10					15		

gta	gtg	gtc	gcc	gtc	gat	aga	ctc	ttc	cac	aac	aaa	atc	tac	aat	cgc	96
Val	Val	Val	Ala	Val	Asp	Arg	Leu	Phe	His	Asn	Lys	Ile	Tyr	Asn	Arg	
			20					25					30			

tac	gtc	aaa	cga	act	tcc	aaa	ttc	atg	gct	cac	gac	gac	aaa	gac	gcc	144
Tyr	Val	Lys	Arg	Thr	Ser	Lys	Phe	Met	Ala	His	Asp	Asp	Lys	Asp	Ala	
		35					40					45				

tgc	aac	atc	ggc	gat	cga	gtg	aag	tta	gat	cca	tca	agg	cct	ttg	agc	192
Cys	Asn	Ile	Gly	Asp	Arg	Val	Lys	Leu	Asp	Pro	Ser	Arg	Pro	Leu	Ser	
	50					55					60					

aag	aat	aag	cat	tgg	att	gtt	gca	gaa	atc	atc	aaa	aaa	gct	cga	att	240
Lys	Asn	Lys	His	Trp	Ile	Val	Ala	Glu	Ile	Ile	Lys	Lys	Ala	Arg	Ile	
65				70					75					80		

tat	tct	cct	aaa	gct	gct	gct	gct	gct	gtt	tct	gct	tct	gct	tct	gct	288
Tyr	Ser	Pro	Lys	Ala	Ala	Ala	Ala	Ala	Val	Ser	Ala	Ser	Ala	Ser	Ala	
			85					90					95			

tcc	tca	gcc	tcc	act	act	gac	tct	tct	gct	cag	tct	cag	att	cct	cca	336
Ser	Ser	Ala	Ser	Thr	Thr	Asp	Ser	Ser	Ala	Gln	Ser	Gln	Ile	Pro	Pro	
			100					105					110			

tca	tct	act	tct	taa												351
Ser	Ser	Thr	Ser													
			115													

<210> 16

<211> 116

<212> PRT

<213> Arabidopsis thaliana

<400> 16

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Met Lys Pro Val Ile Gly Thr Val Val Ser Asn Lys Met Gln Lys Ser
1               5                   10                  15


Val Val Val Ala Val Asp Arg Leu Phe His Asn Lys Ile Tyr Asn Arg
                20                  25                  30


Tyr Val Lys Arg Thr Ser Lys Phe Met Ala His Asp Asp Lys Asp Ala
        35                  40                  45


Cys Asn Ile Gly Asp Arg Val Lys Leu Asp Pro Ser Arg Pro Leu Ser
        50                  55                  60


Lys Asn Lys His Trp Ile Val Ala Glu Ile Ile Lys Lys Ala Arg Ile
65                  70                  75                  80


Tyr Ser Pro Lys Ala Ala Ala Ala Ala Val Ser Ala Ser Ala Ser Ala
                85                  90                  95


Ser Ser Ala Ser Thr Thr Asp Ser Ser Ala Gln Ser Gln Ile Pro Pro
                100                 105                 110


Ser Ser Thr Ser
        115
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<210> 17

<211> 1269

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1269)

<223> 10951

<400> 17
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atg tct tct tct gta gca gtg tta tgg gtt gct act tct tct cta aat        48
Met Ser Ser Ser Val Ala Val Leu Trp Val Ala Thr Ser Ser Leu Asn
1               5                   10                  15


cca gac cca atg aac aat tgt ggg ttg gta agg gtt cta gaa tct tct        96
Pro Asp Pro Met Asn Asn Cys Gly Leu Val Arg Val Leu Glu Ser Ser
```

```
                 20                      25                      30

aga ctg ttc tct cct tgt cag aat cag aga cta aac aaa ggt aag aag     144
Arg Leu Phe Ser Pro Cys Gln Asn Gln Arg Leu Asn Lys Gly Lys Lys
        35                      40                      45

aag cag ata cca act tgg agt tct tct ttt gta agg aac cga agt aga     192
Lys Gln Ile Pro Thr Trp Ser Ser Ser Phe Val Arg Asn Arg Ser Arg
    50                      55                      60

aga att ggt gtt gtg tct tca agc tta gta gca agt cct tct gga gag     240
Arg Ile Gly Val Val Ser Ser Ser Leu Val Ala Ser Pro Ser Gly Glu
65                      70                      75                  80

ata gct ctt tca tct gaa gag aag gtt tac aat gtt gtg ttg aaa caa     288
Ile Ala Leu Ser Ser Glu Glu Lys Val Tyr Asn Val Val Leu Lys Gln
                85                      90                      95

gct gct ttg gtg aac aaa cag cta agg tct tct tct tat gac ctt gat     336
Ala Ala Leu Val Asn Lys Gln Leu Arg Ser Ser Ser Tyr Asp Leu Asp
            100                     105                     110

gtg aag aaa cca caa gat gtt gtt ctt cct ggg agt ttg agt ttg ttg     384
Val Lys Lys Pro Gln Asp Val Val Leu Pro Gly Ser Leu Ser Leu Leu
            115                     120                     125

ggt gaa gct tat gat cga tgc ggt gaa gtt tgc gct gaa tat cct aag     432
Gly Glu Ala Tyr Asp Arg Cys Gly Glu Val Cys Ala Glu Tyr Pro Lys
    130                     135                     140

acg ttt tat ctt gga act ttg ctt atg aca ccc gaa agg cga aag gcg     480
Thr Phe Tyr Leu Gly Thr Leu Leu Met Thr Pro Glu Arg Arg Lys Ala
145                     150                     155                 160

att tgg gca atc tac gtt tgg tgt aga aga act gat gaa ctt gtg gat     528
Ile Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp
                165                     170                     175

ggg cca aat gct tca cat ata act ccc atg gct tta gat aga tgg gaa     576
Gly Pro Asn Ala Ser His Ile Thr Pro Met Ala Leu Asp Arg Trp Glu
            180                     185                     190

gca agg tta gaa gat ctt ttc cgt ggt cgt cct ttc gat atg ctt gat     624
Ala Arg Leu Glu Asp Leu Phe Arg Gly Arg Pro Phe Asp Met Leu Asp
        195                     200                     205

gct gct ctc gct gat aca gtt gct aga tac ccg gtc gat att cag cca     672
Ala Ala Leu Ala Asp Thr Val Ala Arg Tyr Pro Val Asp Ile Gln Pro
        210                     215                     220

ttt cga gac atg atc gaa gga atg aga atg gac ttg aag aaa tcg aga     720
Phe Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Lys Lys Ser Arg
225                     230                     235                 240

tac cag aac ttc gat gat cta tac ctt tac tgc tac tac gtc gct gga     768
Tyr Gln Asn Phe Asp Asp Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly
                245                     250                     255

acc gtc gga ttg atg agc gtt ccg gtt atg gga atc gat cct aag tcg     816
Thr Val Gly Leu Met Ser Val Pro Val Met Gly Ile Asp Pro Lys Ser
```

40

```
                    260                 265                 270

aaa gca aca acc gaa agt gtt tac aac gct gcc ttg gcc ctt ggt ata          864
Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile
            275                 280                 285

gcc aat cag ctt act aac ata ctc aga gac gta ggc gaa gat gcg aga          912
Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg
        290                 295                 300

aga gga agg gtt tat ctg cct cag gat gaa ttg gct cag gct ggt ctt          960
Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu
305                 310                 315                 320

tca gat gaa gac ata ttc gcc gga aaa gta act gat aaa tgg aga aac        1008
Ser Asp Glu Asp Ile Phe Ala Gly Lys Val Thr Asp Lys Trp Arg Asn
                325                 330                 335

ttc atg aaa atg cag ctt aaa cga gca aga atg ttc ttc gac gaa gct        1056
Phe Met Lys Met Gln Leu Lys Arg Ala Arg Met Phe Phe Asp Glu Ala
            340                 345                 350

gag aaa ggc gtc acc gag ctc agt gcc gct agc aga tgg cct gta tgg        1104
Glu Lys Gly Val Thr Glu Leu Ser Ala Ala Ser Arg Trp Pro Val Trp
            355                 360                 365

gct tca ttg cta ttg tac agg aga ata ctg gac gag att gaa gcg aat        1152
Ala Ser Leu Leu Leu Tyr Arg Arg Ile Leu Asp Glu Ile Glu Ala Asn
        370                 375                 380

gat tac aac aat ttt act aag aga gct tat gtg ggg aaa gtc aag aaa        1200
Asp Tyr Asn Asn Phe Thr Lys Arg Ala Tyr Val Gly Lys Val Lys Lys
385                 390                 395                 400

att gca gct ttg cca ttg gct tat gct aaa tca gta cta aag act tca        1248
Ile Ala Ala Leu Pro Leu Ala Tyr Ala Lys Ser Val Leu Lys Thr Ser
                405                 410                 415

agt tca aga cta tcg ata tga                                            1269
Ser Ser Arg Leu Ser Ile
                420
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<210>   18

<211>   422

<212>   PRT

<213>   Arabidopsis thaliana



<400>   18

Met Ser Ser Ser Val Ala Val Leu Trp Val Ala Thr Ser Ser Leu Asn
1               5                   10                  15


Pro Asp Pro Met Asn Asn Cys Gly Leu Val Arg Val Leu Glu Ser Ser
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41

　　　　　　　　　　20　　　　　　　　　　　　　25　　　　　　　　　　　30

Arg Leu Phe Ser Pro Cys Gln Asn Gln Arg Leu Asn Lys Gly Lys Lys
　　　　　　35　　　　　　　　　　40　　　　　　　　　45

Lys Gln Ile Pro Thr Trp Ser Ser Ser Phe Val Arg Asn Arg Ser Arg
　　　　　50　　　　　　　55　　　　　　　　　60

Arg Ile Gly Val Val Ser Ser Ser Leu Val Ala Ser Pro Ser Gly Glu
65　　　　　　　　　70　　　　　　　　75　　　　　　　　80

Ile Ala Leu Ser Ser Glu Glu Lys Val Tyr Asn Val Val Leu Lys Gln
　　　　　　　85　　　　　　　90　　　　　　　　95

Ala Ala Leu Val Asn Lys Gln Leu Arg Ser Ser Ser Tyr Asp Leu Asp
　　　　　　100　　　　　　　105　　　　　　　110

Val Lys Lys Pro Gln Asp Val Val Leu Pro Gly Ser Leu Ser Leu Leu
　　　　115　　　　　　　120　　　　　　　125

Gly Glu Ala Tyr Asp Arg Cys Gly Glu Val Cys Ala Glu Tyr Pro Lys
　　　130　　　　　　　135　　　　　　　140

Thr Phe Tyr Leu Gly Thr Leu Leu Met Thr Pro Glu Arg Arg Lys Ala
145　　　　　　　　150　　　　　　155　　　　　　　160

Ile Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp
　　　　　　　165　　　　　　　170　　　　　　　175

Gly Pro Asn Ala Ser His Ile Thr Pro Met Ala Leu Asp Arg Trp Glu
　　　　　180　　　　　　　185　　　　　　190

Ala Arg Leu Glu Asp Leu Phe Arg Gly Arg Pro Phe Asp Met Leu Asp
　　　　　195　　　　　　200　　　　　　205

Ala Ala Leu Ala Asp Thr Val Ala Arg Tyr Pro Val Asp Ile Gln Pro
　　　　　210　　　　　　215　　　　　　220

Phe Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Lys Lys Ser Arg
225　　　　　　　　230　　　　　　　235　　　　　　　240

Tyr Gln Asn Phe Asp Asp Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly
　　　　　　　245　　　　　　　250　　　　　　　255

Thr Val Gly Leu Met Ser Val Pro Val Met Gly Ile Asp Pro Lys Ser

42

                    260   265   270

Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile
        275   280   285

Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg
        290   295   300

Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu
305   310   315   320

Ser Asp Glu Asp Ile Phe Ala Gly Lys Val Thr Asp Lys Trp Arg Asn
                325   330   335

Phe Met Lys Met Gln Leu Lys Arg Ala Arg Met Phe Phe Asp Glu Ala
            340   345   350

Glu Lys Gly Val Thr Glu Leu Ser Ala Ala Ser Arg Trp Pro Val Trp
            355   360   365

Ala Ser Leu Leu Leu Tyr Arg Arg Ile Leu Asp Glu Ile Glu Ala Asn
        370   375   380

Asp Tyr Asn Asn Phe Thr Lys Arg Ala Tyr Val Gly Lys Val Lys Lys
385   390   395   400

Ile Ala Ala Leu Pro Leu Ala Tyr Ala Lys Ser Val Leu Lys Thr Ser
                405   410   415

Ser Ser Arg Leu Ser Ile
            420

<210>   19

<211>   1125

<212>   DNA

<213>   Arabidopsis thaliana

<220>

<221>   CDS

<222>   (1)..(1125)

43

<223>   12935

<400>   19
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atg gga gca gcg aag aat atc tgg gca tta gcc aac gcc gaa gat gca        48
Met Gly Ala Ala Lys Asn Ile Trp Ala Leu Ala Asn Ala Glu Asp Ala
1               5                   10                  15

gct aac gac gcc gaa caa atc cct tat tct tcg ttc gtc gtc gac acg        96
Ala Asn Asp Ala Glu Gln Ile Pro Tyr Ser Ser Phe Val Val Asp Thr
                20                  25                  30

tct ttg cct ctt cct ctc atg att cct cgt atc ata gag tta tgt aaa       144
Ser Leu Pro Leu Pro Leu Met Ile Pro Arg Ile Ile Glu Leu Cys Lys
            35                  40                  45

gat ctg ttc aag aat tgg gga gag ctt gat gat tca ctc ttc tct gtt       192
Asp Leu Phe Lys Asn Trp Gly Glu Leu Asp Asp Ser Leu Phe Ser Val
        50                  55                  60

gag aga gta tct gga ggc att aca aat ctt ttg ctg aag gtt tct gtg       240
Glu Arg Val Ser Gly Gly Ile Thr Asn Leu Leu Leu Lys Val Ser Val
65                  70                  75                  80

aaa gag gac act aat aaa gaa gtg tct gtt aca gtg aga ctg tat ggg       288
Lys Glu Asp Thr Asn Lys Glu Val Ser Val Thr Val Arg Leu Tyr Gly
                85                  90                  95

cct aac act gag tat gtt att aac cgg gag aga gag att ctg gct atc       336
Pro Asn Thr Glu Tyr Val Ile Asn Arg Glu Arg Glu Ile Leu Ala Ile
                100                 105                 110

aag tat ctc tcg gct gcc gga ttt ggt gcc aag ttg ctt ggt ggt ttt       384
Lys Tyr Leu Ser Ala Ala Gly Phe Gly Ala Lys Leu Leu Gly Gly Phe
            115                 120                 125

gga aat ggc atg gtg caa tcg ttc atc aat gca aga acc tta gag cca       432
Gly Asn Gly Met Val Gln Ser Phe Ile Asn Ala Arg Thr Leu Glu Pro
        130                 135                 140

tca gac atg aga gag cca aag att gct gca caa att gcc aga gaa ctt       480
Ser Asp Met Arg Glu Pro Lys Ile Ala Ala Gln Ile Ala Arg Glu Leu
145                 150                 155                 160

gga aag ttt cat aaa gtg gac ata cca ggt tcc aag gaa cct cag ctg       528
Gly Lys Phe His Lys Val Asp Ile Pro Gly Ser Lys Glu Pro Gln Leu
                165                 170                 175

tgg gtt gat atc ttg aag ttc tat gaa aaa gca tct act ctt acg ttt       576
Trp Val Asp Ile Leu Lys Phe Tyr Glu Lys Ala Ser Thr Leu Thr Phe
                180                 185                 190

gaa gaa cct gat aag cag aag ctc ttt gag act att tcg ttt gaa gaa       624
Glu Glu Pro Asp Lys Gln Lys Leu Phe Glu Thr Ile Ser Phe Glu Glu
            195                 200                 205

ctc cac aaa gaa att att gag cta agg gaa ttc aca ggc tta ctt aac       672
Leu His Lys Glu Ile Ile Glu Leu Arg Glu Phe Thr Gly Leu Leu Asn
        210                 215                 220
```

44

```
gca cct gtg gtg ttt gct cat aac gat tta cta tca gga aac ttc atg      720
Ala Pro Val Val Phe Ala His Asn Asp Leu Leu Ser Gly Asn Phe Met
225                 230             235                 240

ctg aat gat gaa gaa gag aaa cta tac ttg att gat ttc gag tat gga      768
Leu Asn Asp Glu Glu Glu Lys Leu Tyr Leu Ile Asp Phe Glu Tyr Gly
                    245             250                 255

tca tac aac tat aga ggc ttt gac atc gga aat cac ttc aat gaa tat      816
Ser Tyr Asn Tyr Arg Gly Phe Asp Ile Gly Asn His Phe Asn Glu Tyr
            260             265                 270

gca gga tac gac tgt gat tac agc ctg tac cca agt aaa gag gaa caa      864
Ala Gly Tyr Asp Cys Asp Tyr Ser Leu Tyr Pro Ser Lys Glu Glu Gln
            275             280                 285

tat cat ttc atc aag cat tac tta cag cca gac aaa cca gac gag gtc      912
Tyr His Phe Ile Lys His Tyr Leu Gln Pro Asp Lys Pro Asp Glu Val
            290             295                 300

agt atc gct gaa gta gaa tca gtc ttt gta gag aca gat gcg tat aaa      960
Ser Ile Ala Glu Val Glu Ser Val Phe Val Glu Thr Asp Ala Tyr Lys
305                 310             315                 320

tta gca tct cat ttg tac tgg gca ata tgg gcg atc atc cag gca agg     1008
Leu Ala Ser His Leu Tyr Trp Ala Ile Trp Ala Ile Ile Gln Ala Arg
                    325             330                 335

atg tct ccc att gag ttt gaa tat ttg ggt tac ttc ttt ttg cgg tac     1056
Met Ser Pro Ile Glu Phe Glu Tyr Leu Gly Tyr Phe Phe Leu Arg Tyr
                340             345                 350

aat gaa tac aag aag cag aag cca ctt act ttt tca ctt gtt aca tct     1104
Asn Glu Tyr Lys Lys Gln Lys Pro Leu Thr Phe Ser Leu Val Thr Ser
                355             360                 365

cac ctc tca gca tcg ctg tag                                         1125
His Leu Ser Ala Ser Leu
        370
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<210>  20

<211>  374

<212>  PRT

<213>  Arabidopsis thaliana


<400>  20

Met Gly Ala Ala Lys Asn Ile Trp Ala Leu Ala Asn Ala Glu Asp Ala
1               5                   10                  15


Ala Asn Asp Ala Glu Gln Ile Pro Tyr Ser Ser Phe Val Val Asp Thr
            20                  25                  30
```

45

```
Ser Leu Pro Leu Pro Leu Met Ile Pro Arg Ile Ile Glu Leu Cys Lys
        35                  40                  45

Asp Leu Phe Lys Asn Trp Gly Glu Leu Asp Asp Ser Leu Phe Ser Val
        50                  55                  60

Glu Arg Val Ser Gly Gly Ile Thr Asn Leu Leu Leu Lys Val Ser Val
65                  70                  75                  80

Lys Glu Asp Thr Asn Lys Glu Val Ser Val Thr Val Arg Leu Tyr Gly
                85                  90                  95

Pro Asn Thr Glu Tyr Val Ile Asn Arg Glu Arg Glu Ile Leu Ala Ile
                100                 105                 110

Lys Tyr Leu Ser Ala Ala Gly Phe Gly Ala Lys Leu Leu Gly Gly Phe
            115                 120                 125

Gly Asn Gly Met Val Gln Ser Phe Ile Asn Ala Arg Thr Leu Glu Pro
    130                 135                 140

Ser Asp Met Arg Glu Pro Lys Ile Ala Ala Gln Ile Ala Arg Glu Leu
145                 150                 155                 160

Gly Lys Phe His Lys Val Asp Ile Pro Gly Ser Lys Glu Pro Gln Leu
                165                 170                 175

Trp Val Asp Ile Leu Lys Phe Tyr Glu Lys Ala Ser Thr Leu Thr Phe
            180                 185                 190

Glu Glu Pro Asp Lys Gln Lys Leu Phe Glu Thr Ile Ser Phe Glu Glu
        195                 200                 205

Leu His Lys Glu Ile Ile Glu Leu Arg Glu Phe Thr Gly Leu Leu Asn
    210                 215                 220

Ala Pro Val Val Phe Ala His Asn Asp Leu Leu Ser Gly Asn Phe Met
225                 230                 235                 240

Leu Asn Asp Glu Glu Glu Lys Leu Tyr Leu Ile Asp Phe Glu Tyr Gly
                245                 250                 255

Ser Tyr Asn Tyr Arg Gly Phe Asp Ile Gly Asn His Phe Asn Glu Tyr
                260                 265                 270
```

46

```
Ala Gly Tyr Asp Cys Asp Tyr Ser Leu Tyr Pro Ser Lys Glu Glu Gln
        275             280             285


Tyr His Phe Ile Lys His Tyr Leu Gln Pro Asp Lys Pro Asp Glu Val
    290             295             300


Ser Ile Ala Glu Val Glu Ser Val Phe Val Glu Thr Asp Ala Tyr Lys
305             310             315             320


Leu Ala Ser His Leu Tyr Trp Ala Ile Trp Ala Ile Ile Gln Ala Arg
                325             330             335


Met Ser Pro Ile Glu Phe Glu Tyr Leu Gly Tyr Phe Phe Leu Arg Tyr
            340             345             350


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47

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        .65                  70                  75                  80

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        Gln Phe Phe Pro Leu Ala Ala Val Val Gly Gln Glu Gly Ile Lys Thr
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        gct ctt tta ctt ggc gcg gtt gat cgt gaa atc gga ggg att gcc att        336
        Ala Leu Leu Leu Gly Ala Val Asp Arg Glu Ile Gly Gly Ile Ala Ile
                        100                 105                 110

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        gaa atc ctc cct cct att gaa gtt gtt gta ggc tca ata tca aat gct        432
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        gag tac aat gct gac aat acc att aag act gag att gtc aaa tct cct        528
        Glu Tyr Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro
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        ttc att cag att cca cta gga gtt aca gaa gac aga ctc att ggg tct        576
        Phe Ile Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser
                        180                 185                 190

        gtt gat gtt gag gag tct gtg aaa agg ggg aca act gtt ttc caa cct        624
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                            245                 250                 255

        tgc aaa cca ctt tta att gca acc tat aac cct gaa gaa ggt gct gtt        816
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                        260                 265                 270

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48

Text deleted

Text deleted

Text deleted

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CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,
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(54) Title: NUCLEIC ACID MOLECULES ENCODING PROTEINS ESSENTIAL FOR PLANT GROWTH

(57) Abstract: Nucleotide sequences are isolated from *Arabidopsis thaliana* that code for proteins essential for plant growth and
developement. The essentially of the proteins may be exploited by recombinantly expressing the proteins and using them in screening
assays to identify compounds that interact with or inhibit the proteins and are therefore potential herbicides.

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7   G01N33/68   C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7   C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data, PAJ, Sequence Search, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL [Online] 1 March 2001 (2001-03-01), XP002253634 accession no. EBI Database accession no. Q9FKB8 abstract & KOTANI, H. ET AL: "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned P1 and TAC clones." DNA RES., 1998, pages 203-216, the whole document -----	1-10
A	WO 00/42205 A (NOVARTIS ERFIND VERWALT GMBH ;NOVARTIS AG (CH); BUDZISZEWSKI GREGO) 20 July 2000 (2000-07-20) abstract; claims 39-44 -----	1-10

-/--

[X] Further documents are listed in the continuation of box C.   [X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 October 2003	2 0. 01. 04

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Luis Alves, D

Form PCT/ISA/210 (second sheet) (July 1992)

page 1 of 2

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; June 2001 (2001-06), WILLIAMS MARK A ET AL: "Characterization and inhibition of chloroplast-localized peptide deformylases from Arabidopsis thaliana" XP002253632 Database accession no. PREV200100419457 abstract & HORTSCIENCE, vol. 36, no. 3, June 2001 (2001-06), page 554, 98th Annual International Conference of the American Society for Horticultural Science;Sacramento, California, USA; July 21-25, 2001 ISSN: 0018-5345 -----	1-10
A	ITO TAKUYA ET AL: "Regional insertional mutagenesis of genes on Arabidopsis thaliana chromosome V using the Ac/Ds transposon in combination with a cDNA scanning method." PLANT JOURNAL, vol. 17, no. 4, February 1999 (1999-02), pages 433-444, XP002253633 ISSN: 0960-7412 the whole document -----	1-10
A	WO 00/15809 A (NOVARTIS ERFIND VERWALT GMBH ;NOVARTIS AG (CH); BUDZISZEWSKI GREGO) 23 March 2000 (2000-03-23) abstract page 8, paragraph 3 - page 17, last paragraph -----	1-10

INTERNATIONAL SEARCH REPORT

| Box I | Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet) |

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

| Box II | Observations where unity of invention is lacking (Continuation of item 2 of first sheet) |

This International Searching Authority found multiple inventions in this international application, as follows:

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see additional sheet
```

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

```
see PCT/ISA/210 annex
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Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

This International Searching Authority found multiple (groups of)
inventions in this international application, as follows:

1. claims: 1-10 (all partially)

> Invention 1

> Screening methods for herbicidal compounds comprising
> identifying ligands or inhibitors of the protein having SEQ
> Id No 2.
> ---

2. claims: 1-10 (all partially)

> Inventions 2 to 48

> Screening methods for herbicidal compounds comprising
> identifying ligands or inhibitors of the protein having SEQ
> Id No n (with n=4...96, n being an even number).
> ---

International Application No

PCT/EP 02/07929

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 0042205	A	20-07-2000	AU	2290900 A	01-08-2000
			CA	2362484 A1	20-07-2000
			CN	1341151 T	20-03-2002
			WO	0042205 A2	20-07-2000
			EP	1141344 A2	10-10-2001
			JP	2002534128 T	15-10-2002
WO 0015809	A	23-03-2000	AU	6082399 A	03-04-2000
			CA	2340332 A1	23-03-2000
			CN	1318106 T	17-10-2001
			WO	0015809 A2	23-03-2000
			EP	1114168 A2	11-07-2001
			JP	2002525061 T	13-08-2002

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305                 310                 315                 320
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gaa aca gca aag acg cag att ata ttg gct aga gaa tat ttg aaa gat     1008
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cga ggt ggt gtc cag gga cac cgc gcc gaa ttg tat gca gct cgt gtg     1104
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        370                 375                 380
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385                 390                 395                 400
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                    405                 410                 415
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cct cca caa aat agc gaa tct gga gaa gaa gaa aat gaa gaa gaa caa     1296
Pro Pro Gln Asn Ser Glu Ser Gly Glu Glu Glu Asn Glu Glu Glu Gln
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gaa gaa gaa gaa gag gat gaa agc aat gaa gaa aat gaa aat gag cag     1344
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ctg gtg gat gag aaa ctc ctc ttc ttt gct caa caa gcc cag aaa cgt     1440
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gct gtg gat gca acc ctt aga gca gct gca cca tac cag aaa ttg cgc     1584
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49

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aga gag aag gat atc tca gga act agg aaa gtc ttt gtt gag aag aca      1632
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    530                 535                 540

gat atg agg gcc aaa aga atg gca agg aaa gct gga gcc ctg gtt atc      1680
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545                 550                 555                 560

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Phe Val Val Asp Ala Ser Gly Ser Met Ala Leu Asn Arg Met Gln Asn
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gcc aaa ggt gct gca ctc aaa cta ctg gca gag agc tat act agc agg      1776
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gat cag gtt tcg att att cct ttc cga ggg gat gct gcg gaa gtg ctc      1824
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Leu Pro Cys Gly Gly Gly Ser Pro Leu Ala His Gly Leu Thr Thr Ala
625                 630                 635                 640

gta aga gta gga ctt aac gca gag aag agt ggt gat gtc ggg cgc ata      1968
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                645                 650                 655

atg att gtt gcg ata acc gat ggt cga gcc aac att aca ctg aaa aga      2016
Met Ile Val Ala Ile Thr Asp Gly Arg Ala Asn Ile Thr Leu Lys Arg
                660                 665                 670

tca act gat ccg gag tct att gcc cca gat gct cct aga ccc acg tcc      2064
Ser Thr Asp Pro Glu Ser Ile Ala Pro Asp Ala Pro Arg Pro Thr Ser
                675                 680                 685

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Lys Glu Leu Lys Asp Glu Ile Leu Glu Val Ala Gly Lys Ile Tyr Lys
        690                 695                 700

gca ggg atg tct ctt cta gtg att gat acc gag aac aag ttt gtt tca      2160
Ala Gly Met Ser Leu Leu Val Ile Asp Thr Glu Asn Lys Phe Val Ser
705                 710                 715                 720

act ggt ttt gca aag gag atc gca aga gtt gct caa gga aaa tat tat      2208
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                725                 730                 735

tac ttg cca aat gct tcg gat gct gta atc tcg gcc acc act agg gat      2256
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                740                 745                 750

gca cta tct gat ctg aag aat tct tga                                  2283
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<213>   Arabidopsis thaliana

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            20              25                  30


Leu Ser Leu Pro Lys Arg Asn Arg Ile Ala Ser Cys Arg Phe Thr Val
        35                  40                  45


Arg Ala Ser Ala Asn Ala Thr Val Glu Ser Pro Asn Gly Val Pro Ala
    50                  55                  60


Ser Thr Ser Asp Thr Asp Thr Glu Thr Asp Thr Thr Ser Tyr Gly Arg
65                  70                  75                  80


Gln Phe Phe Pro Leu Ala Ala Val Val Gly Gln Glu Gly Ile Lys Thr
                85                  90                  95


Ala Leu Leu Leu Gly Ala Val Asp Arg Glu Ile Gly Gly Ile Ala Ile
            100                 105                 110


Ser Gly Arg Arg Gly Thr Ala Lys Thr Val Met Ala Arg Gly Leu His
        115                 120                 125


Glu Ile Leu Pro Pro Ile Glu Val Val Val Gly Ser Ile Ser Asn Ala
    130                 135                 140


Asp Pro Ala Cys Pro Asp Glu Trp Glu Asp Asp Leu Asp Glu Arg Ile
145                 150                 155                 160


Glu Tyr Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro
                165                 170                 175
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51

Phe Ile Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser
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Val Asp Val Glu Glu Ser Val Lys Arg Gly Thr Thr Val Phe Gln Pro
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Gly Leu Leu Ala Glu Ala His Arg Gly Val Leu Tyr Val Asp Glu Ile
     210   215   220

Asn Leu Leu Asp Glu Gly Ile Ser Asn Leu Leu Leu Asn Val Leu Thr
225   230   235   240

Asp Gly Val Asn Ile Val Glu Arg Glu Gly Ile Ser Phe Arg His Pro
            245   250   255

Cys Lys Pro Leu Leu Ile Ala Thr Tyr Asn Pro Glu Glu Gly Ala Val
         260   265   270

Arg Glu His Leu Leu Asp Arg Val Ala Ile Asn Leu Ser Ala Asp Leu
        275   280   285

Pro Met Ser Phe Glu Asp Arg Val Ala Ala Val Gly Ile Ala Thr Gln
    290   295   300

Phe Gln Glu Arg Cys Asn Glu Val Phe Arg Met Val Asn Glu Glu Thr
305   310   315   320

Glu Thr Ala Lys Thr Gln Ile Ile Leu Ala Arg Glu Tyr Leu Lys Asp
          325   330   335

Val Lys Ile Ser Arg Glu Gln Leu Lys Tyr Leu Val Leu Glu Ala Val
         340   345   350

Arg Gly Gly Val Gln Gly His Arg Ala Glu Leu Tyr Ala Ala Arg Val
        355   360   365

Ala Lys Cys Leu Ala Ala Ile Glu Gly Arg Glu Lys Val Thr Ile Asp
    370   375   380

Asp Leu Arg Lys Ala Val Glu Leu Val Ile Leu Pro Arg Ser Ser Leu
385   390   395   400

Asp Glu Thr Pro Pro Glu Gln Gln Asn Gln Pro Pro Pro Pro Pro Pro
          405   410   415

52

```
Pro Pro Gln Asn Ser Glu Ser Gly Glu Glu Glu Asn Glu Glu Glu Gln
        420             425                 430
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```
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```
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        450             455                 460
```

```
Leu Val Asp Glu Lys Leu Leu Phe Phe Ala Gln Gln Ala Gln Lys Arg
465                 470             475                 480
```

```
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```

```
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```

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Ala Lys Gly Ala Ala Leu Lys Leu Leu Ala Glu Ser Tyr Thr Ser Arg
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Asp Gln Val Ser Ile Ile Pro Phe Arg Gly Asp Ala Ala Glu Val Leu
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```

```
Leu Pro Pro Ser Arg Ser Ile Ala Met Ala Arg Asn Arg Leu Glu Arg
        610             615                 620
```

```
Leu Pro Cys Gly Gly Gly Ser Pro Leu Ala His Gly Leu Thr Thr Ala
625                 630                 635             640
```

```
Val Arg Val Gly Leu Asn Ala Glu Lys Ser Gly Asp Val Gly Arg Ile
                645                 650                 655
```

53

```
Met Ile Val Ala Ile Thr Asp Gly Arg Ala Asn Ile Thr Leu Lys Arg
            660                 665                 670

Ser Thr Asp Pro Glu Ser Ile Ala Pro Asp Ala Pro Arg Pro Thr Ser
            675                 680                 685

Lys Glu Leu Lys Asp Glu Ile Leu Glu Val Ala Gly Lys Ile Tyr Lys
            690                 695                 700

Ala Gly Met Ser Leu Leu Val Ile Asp Thr Glu Asn Lys Phe Val Ser
705                 710                 715                 720

Thr Gly Phe Ala Lys Glu Ile Ala Arg Val Ala Gln Gly Lys Tyr Tyr
                725                 730                 735

Tyr Leu Pro Asn Ala Ser Asp Ala Val Ile Ser Ala Thr Thr Arg Asp
                740                 745                 750

Ala Leu Ser Asp Leu Lys Asn Ser
                755                 760
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<210> 23

<211> 1167

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1167)

<223> 14519

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atg gcg ttt ttt aag cta ctt ttg ttt ctt ttt ctc gta acg ctc caa    48
Met Ala Phe Phe Lys Leu Leu Leu Phe Leu Phe Leu Val Thr Leu Gln
1               5                   10                  15

att gct tca ttc act gga aat gga gaa gct tct tct tct tcc tca gag    96
Ile Ala Ser Phe Thr Gly Asn Gly Glu Ala Ser Ser Ser Ser Ser Glu
                20                  25                  30

aac aat ggc tgc aat gga gat caa aac cat ttg ctt aac gaa ctc aaa   144
Asn Asn Gly Cys Asn Gly Asp Gln Asn His Leu Leu Asn Glu Leu Lys
            35                  40                  45
```

54

```
tcc acc gtc tct gct ctt caa tca atc atc aag gag aaa aac caa gaa        192
Ser Thr Val Ser Ala Leu Gln Ser Ile Ile Lys Glu Lys Asn Gln Glu
    50                  55                  60

ttg ctt agc aag gaa gag aaa atc cga ggt ttg gag tta tat atc agg        240
Leu Leu Ser Lys Glu Glu Lys Ile Arg Gly Leu Glu Leu Tyr Ile Arg
65                  70                  75                  80

gag aaa cct tat ttg ttt gag agt gaa att gat ttt tct caa ttt gag        288
Glu Lys Pro Tyr Leu Phe Glu Ser Glu Ile Asp Phe Ser Gln Phe Glu
                85                  90                  95

aat ccg gta aag cat gcg agt gaa gta gaa gag aag gtt tat gaa cta        336
Asn Pro Val Lys His Ala Ser Glu Val Glu Glu Lys Val Tyr Glu Leu
                100                 105                 110

cag aaa cag gta ttt gga tta aaa cgg gaa gtg gaa acg caa cgc aag        384
Gln Lys Gln Val Phe Gly Leu Lys Arg Glu Val Glu Thr Gln Arg Lys
            115                 120                 125

aga agg ctc gaa gtg gaa gct gaa tta gca gat aag aaa gtt gca caa        432
Arg Arg Leu Glu Val Glu Ala Glu Leu Ala Asp Lys Lys Val Ala Gln
        130                 135                 140

ctt agc tca aag ctt gaa aat atc gat ggg tgg ttc ttg tct aaa ctt        480
Leu Ser Ser Lys Leu Glu Asn Ile Asp Gly Trp Phe Leu Ser Lys Leu
145                 150                 155                 160

ggt ctt aac ccg act gaa agt cag gca tat ctg atg acc cta tgg cat        528
Gly Leu Asn Pro Thr Glu Ser Gln Ala Tyr Leu Met Thr Leu Trp His
                165                 170                 175

caa cat ctt agc cca act ctt cat acc act ctt caa atg gtg tcg atg        576
Gln His Leu Ser Pro Thr Leu His Thr Thr Leu Gln Met Val Ser Met
                180                 185                 190

aaa att gag caa gtc cag aaa tgg tca gag cct cac att gaa aca ctg        624
Lys Ile Glu Gln Val Gln Lys Trp Ser Glu Pro His Ile Glu Thr Leu
            195                 200                 205

aac tca caa tgg att cca agc atc aaa gat gca tgt gtc aca ata acc        672
Asn Ser Gln Trp Ile Pro Ser Ile Lys Asp Ala Cys Val Thr Ile Thr
        210                 215                 220

ata tat ctc gaa cca aaa gtt caa tat ata acc gat aag tcc atc gag        720
Ile Tyr Leu Glu Pro Lys Val Gln Tyr Ile Thr Asp Lys Ser Ile Glu
225                 230                 235                 240

ttg tta tat aca tct aag cag gct ttg aca cca cat ctc atc caa gga        768
Leu Leu Tyr Thr Ser Lys Gln Ala Leu Thr Pro His Leu Ile Gln Gly
                245                 250                 255

ttt gac gct tca tac tac tat ctt gag gtg atc aga aca cat aca cat        816
Phe Asp Ala Ser Tyr Tyr Tyr Leu Glu Val Ile Arg Thr His Thr His
                260                 265                 270

ccg tac acg acc cgg att atg acc tta acg aag cca cac ttg gag aga        864
Pro Tyr Thr Thr Arg Ile Met Thr Leu Thr Lys Pro His Leu Glu Arg
            275                 280                 285
```

55

```
gta caa gtt gcc tta gag cca tat act gaa aac gta aga cat ggc ttt          912
Val Gln Val Ala Leu Glu Pro Tyr Thr Glu Asn Val Arg His Gly Phe
290                     295                 300

cag aag ttg gtt aac tca acc aaa atc tac cat caa cag gct caa gaa          960
Gln Lys Leu Val Asn Ser Thr Lys Ile Tyr His Gln Gln Ala Gln Glu
305                     310                 315                 320

atg ctg aag aac aat gag atc acc aaa ccg gtt gct acc atg gac tta         1008
Met Leu Lys Asn Asn Glu Ile Thr Lys Pro Val Ala Thr Met Asp Leu
                325                 330                 335

gct tgg gtt ggg gcc aca gct tta att gga ttc cct ctt ata ttc atc        1056
Ala Trp Val Gly Ala Thr Ala Leu Ile Gly Phe Pro Leu Ile Phe Ile
                340                 345                 350

atc aaa ttg ctt tct gca gtc tcc aat cct aag ggg aag aag aga cac        1104
Ile Lys Leu Leu Ser Ala Val Ser Asn Pro Lys Gly Lys Lys Arg His
                355                 360                 365

aac cat aaa aaa gaa cca acc acc ggg tac cgc aga gcc aaa cgc cga        1152
Asn His Lys Lys Glu Pro Thr Thr Gly Tyr Arg Arg Ala Lys Arg Arg
370                     375                 380

                                                                        1167

cat cct cac caa tga
His Pro His Gln
385
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<210> 24

<211> 388

<212> PRT

<213> Arabidopsis thaliana

<400> 24

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Met Ala Phe Phe Lys Leu Leu Leu Phe Leu Phe Leu Val Thr Leu Gln
1               5               10                  15

Ile Ala Ser Phe Thr Gly Asn Gly Glu Ala Ser Ser Ser Ser Ser Glu
        20                  25                  30

Asn Asn Gly Cys Asn Gly Asp Gln Asn His Leu Leu Asn Glu Leu Lys
        35                  40                  45

Ser Thr Val Ser Ala Leu Gln Ser Ile Ile Lys Glu Lys Asn Gln Glu
        50                  55                  60

Leu Leu Ser Lys Glu Glu Lys Ile Arg Gly Leu Glu Leu Tyr Ile Arg
65                  70                  75                  80
```

56

Glu Lys Pro Tyr Leu Phe Glu Ser Glu Ile Asp Phe Ser Gln Phe Glu
                85   90   95

Asn Pro Val Lys His Ala Ser Glu Val Glu Glu Lys Val Tyr Glu Leu
              ·100   105   110

Gln Lys Gln Val Phe Gly Leu Lys Arg Glu Val Glu Thr Gln Arg Lys
            115   120   125

Arg Arg Leu Glu Val Glu Ala Glu Leu Ala Asp Lys Lys Val Ala Gln
    130   135   140

Leu Ser Ser Lys Leu Glu Asn Ile Asp Gly Trp Phe Leu Ser Lys Leu
145   150   155   160

Gly Leu Asn Pro Thr Glu Ser Gln Ala Tyr Leu Met Thr Leu Trp His
              165   170   175

Gln His Leu Ser Pro Thr Leu His Thr Thr Leu Gln Met Val Ser Met
              180   185   190

Lys Ile Glu Gln Val Gln Lys Trp Ser Glu Pro His Ile Glu Thr Leu·
        195   200   205

Asn Ser Gln Trp Ile Pro Ser Ile Lys Asp Ala Cys Val Thr Ile Thr
    210   215   220

Ile Tyr Leu Glu Pro Lys Val Gln Tyr Ile Thr Asp Lys Ser Ile Glu
225   230   235   240

Leu Leu Tyr Thr Ser Lys Gln Ala Leu Thr Pro His Leu Ile Gln Gly
              245   250   255

Phe Asp Ala Ser Tyr Tyr Tyr Leu Glu Val Ile Arg Thr His Thr His
              260   265   270

Pro Tyr Thr Thr Arg Ile Met Thr Leu Thr Lys Pro His Leu Glu Arg
        275   280   285

Val Gln Val Ala Leu Glu Pro Tyr Thr Glu Asn Val Arg His Gly Phe
    290   295   300

Gln Lys Leu Val Asn Ser Thr Lys Ile Tyr His Gln Gln Ala Gln Glu
305   310   315   320

```
Met Leu Lys Asn Asn Glu Ile Thr Lys Pro Val Ala Thr Met Asp Leu
              325                 330                 335
```

```
Ala Trp Val Gly Ala Thr Ala Leu Ile Gly Phe Pro Leu Ile Phe Ile
              340                 345                 350
```

```
Ile Lys Leu Leu Ser Ala Val Ser Asn Pro Lys Gly Lys Lys Arg His
              355                 360                 365
```

```
Asn His Lys Lys Glu Pro Thr Thr Gly Tyr Arg Arg Ala Lys Arg Arg
    370                 375                 380
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His Pro His Gln
385
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<210> 25

<211> 2463

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2463)

<223> 14610.1


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<400> 25
atg ggg agg aga ggt cgc ggc ggc ggc ggt ggt atg ggc gga gga atc      48
Met Gly Arg Arg Gly Arg Gly Gly Gly Gly Gly Met Gly Gly Gly Ile
1               5                   10                  15
```

```
aat cgt aga tat ctg agt caa gtt atg gat acg tgc ggc aag gat tta      96
Asn Arg Arg Tyr Leu Ser Gln Val Met Asp Thr Cys Gly Lys Asp Leu
              20                  25                  30
```

```
tct acg gcg gag gac atc gtt gat gat ctt cgt tcc agg tac ggc aat     144
Ser Thr Ala Glu Asp Ile Val Asp Asp Leu Arg Ser Arg Tyr Gly Asn
              35                  40                  45
```

```
ttt gcg agg ttg act cgg caa gtg ctt cta ctc aat gtc agg caa gtc     192
Phe Ala Arg Leu Thr Arg Gln Val Leu Leu Leu Asn Val Arg Gln Val
    50                  55                  60
```

```
ctt aat gtt aga aac aac aag agg gtt aaa gac gaa gat gaa gat gac     240
```

```
Leu Asn Val Arg Asn Asn Lys Arg Val Lys Asp Glu Asp Glu Asp Asp
65                  70              75                  80

aac att gga gat gag gaa ggt tct gct tct cag agg aag aaa cag aga     288
Asn Ile Gly Asp Glu Glu Gly Ser Ala Ser Gln Arg Lys Lys Gln Arg
                        85              90                  95

cgg gtt gat gag aaa gag gag aaa ttg cag cga gcg gag cag tcg cat     336
Arg Val Asp Glu Lys Glu Glu Lys Leu Gln Arg Ala Glu Gln Ser His
                100             105             110

tta agg aag agg aat atg gaa cgt tca gtg tct tct tct ccg tct tct     384
Leu Arg Lys Arg Asn Met Glu Arg Ser Val Ser Ser Ser Pro Ser Ser
            115             120                 125

tct tct tct tcg gaa gac agt ggt gat gtg tcg act tct gag gac gcg     432
Ser Ser Ser Ser Glu Asp Ser Gly Asp Val Ser Thr Ser Glu Asp Ala
        130                 135                 140

gtt tat ggc gag aag ctg agt ccg ccg cgg ttt gat ctg atc aat gac     480
Val Tyr Gly Glu Lys Leu Ser Pro Pro Arg Phe Asp Leu Ile Asn Asp
145                 150                 155                 160

agt cta aga gat aac tac gct aag ttg aac agc tcc tcg aag aaa cca     528
Ser Leu Arg Asp Asn Tyr Ala Lys Leu Asn Ser Ser Ser Lys Lys Pro
                165             170                 175

att ggg tcg cct gcg gaa aag aat gtg gaa gtt gag act gtg agc aac     576
Ile Gly Ser Pro Ala Glu Lys Asn Val Glu Val Glu Thr Val Ser Asn
            180                 185             190

aaa ggt aga agc aag ttg gct aca atg ggg gcc aga aag gag gct aaa     624
Lys Gly Arg Ser Lys Leu Ala Thr Met Gly Ala Arg Lys Glu Ala Lys
            195             200             205

gtt tct ctt tcc ctc agt gga gct act ggt aat ggt gat ttg gaa gtt     672
Val Ser Leu Ser Leu Ser Gly Ala Thr Gly Asn Gly Asp Leu Glu Val
        210             215                 220

gag ggt act aaa gga cct act ttt aaa gac ttt ggt ggg att aag aaa     720
Glu Gly Thr Lys Gly Pro Thr Phe Lys Asp Phe Gly Gly Ile Lys Lys
225                 230                 235                 240

ata ttg gat gaa ttg gag atg aat gtt cta ttc ccc att ctc aat cct     768
Ile Leu Asp Glu Leu Glu Met Asn Val Leu Phe Pro Ile Leu Asn Pro
                    245             250                 255

gag ccg ttt aag aag att gga gtg aag cca cca agt ggg att cta ttt     816
Glu Pro Phe Lys Lys Ile Gly Val Lys Pro Pro Ser Gly Ile Leu Phe
            260                 265                 270

cat gga cca cct ggc tgt ggg aag act aag ttg gcc aat gcc att gcc     864
His Gly Pro Pro Gly Cys Gly Lys Thr Lys Leu Ala Asn Ala Ile Ala
            275                 280                 285

aat gaa gct ggt gtt ccg ttt tat aag att tca gcc aca gag gtg att     912
Asn Glu Ala Gly Val Pro Phe Tyr Lys Ile Ser Ala Thr Glu Val Ile
            290                 295                 300

tct ggt gtt tct ggt gct tct gaa gag aat atc aga gag ctc ttt tct     960
```

59

```
Ser Gly Val Ser Gly Ala Ser Glu Glu Asn Ile Arg Glu Leu Phe Ser
305              310              315              320

aaa gca tat agg act gcg cct tcg att gtg ttt atc gat gag att gat    1008
Lys Ala Tyr Arg Thr Ala Pro Ser Ile Val Phe Ile Asp Glu Ile Asp
                325              330              335

gcg att ggt tca aag aga gag aat cag caa aga gag atg gag aag cgg    1056
Ala Ile Gly Ser Lys Arg Glu Asn Gln Gln Arg Glu Met Glu Lys Arg
            340              345              350

ata gta aca caa ttg ttg act tgt atg gat gga cct ggt aac aaa ggc    1104
Ile Val Thr Gln Leu Leu Thr Cys Met Asp Gly Pro Gly Asn Lys Gly
        355              360              365

gat aaa aat gct cct gat tct agt gct ggt ttt gtt ctt gtc att gga    1152
Asp Lys Asn Ala Pro Asp Ser Ser Ala Gly Phe Val Leu Val Ile Gly
    370              375              380

gct aca aat agg cct gat gct ctt gat cct gct ttg agg aga agt gga    1200
Ala Thr Asn Arg Pro Asp Ala Leu Asp Pro Ala Leu Arg Arg Ser Gly
385              390              395              400

cga ttt gaa act gag atc gct cta act gct cca gat gaa gac gca agg    1248
Arg Phe Glu Thr Glu Ile Ala Leu Thr Ala Pro Asp Glu Asp Ala Arg
            405              410              415

gct gag ata ctc tct gtt gta gcc caa aaa ctt aga tta gaa gga ccc    1296
Ala Glu Ile Leu Ser Val Val Ala Gln Lys Leu Arg Leu Glu Gly Pro
        420              425              430

ttt gac aag aaa aga ata gct cgt tta aca ccg ggt ttt gtt gga gct    1344
Phe Asp Lys Lys Arg Ile Ala Arg Leu Thr Pro Gly Phe Val Gly Ala
    435              440              445

gat ttg gag agt gtt gct tac ttg gct ggc agg aaa gcc att aag aga    1392
Asp Leu Glu Ser Val Ala Tyr Leu Ala Gly Arg Lys Ala Ile Lys Arg
    450              455              460

atc ttg gat tca agg aaa tct gaa cag tct ggg gac ggt gaa gac gat    1440
Ile Leu Asp Ser Arg Lys Ser Glu Gln Ser Gly Asp Gly Glu Asp Asp
465              470              475              480

aaa tct tgg ctg agg atg ccc tgg cca gaa gaa gag ttg gaa aag ctc    1488
Lys Ser Trp Leu Arg Met Pro Trp Pro Glu Glu Glu Leu Glu Lys Leu
            485              490              495

ttt gtc aaa atg tct gat ttc gag gaa gca gtg aat cta gtt cag gca    1536
Phe Val Lys Met Ser Asp Phe Glu Glu Ala Val Asn Leu Val Gln Ala
        500              505              510

tct tta aca aga gaa gga ttc tct atc gtg cct gat gtc aag tgg gat    1584
Ser Leu Thr Arg Glu Gly Phe Ser Ile Val Pro Asp Val Lys Trp Asp
        515              520              525

gat gtt ggt gga ctt gac cat cta cga ctt caa ttc aac cgt tat ata    1632
Asp Val Gly Gly Leu Asp His Leu Arg Leu Gln Phe Asn Arg Tyr Ile
    530              535              540

gtg agg cct atc aaa aag cct gat att tat aag gct ttt ggg gta gac    1680
```

Val Arg Pro Ile Lys Lys Pro Asp Ile Tyr Lys Ala Phe Gly Val Asp
545   550   555   560

tta gag aca ggg ttt ttg ctc tat gga cca ccg ggt tgt ggc aag aca   1728
Leu Glu Thr Gly Phe Leu Leu Tyr Gly Pro Pro Gly Cys Gly Lys Thr
                565   570   575

ttg att gca aag gca gct gct aac gag gct gga gct aat ttc atg cac   1776
Leu Ile Ala Lys Ala Ala Ala Asn Glu Ala Gly Ala Asn Phe Met His
                580   585   590

atc aag ggt gcc gaa ctt cta aat aaa tac gtt gga gaa agt gag ctt   1824
Ile Lys Gly Ala Glu Leu Leu Asn Lys Tyr Val Gly Glu Ser Glu Leu
                595   600   605

gct att cgt acg ttg ttt cag cga gct cgg aca tgt gca cca tgt gta   1872
Ala Ile Arg Thr Leu Phe Gln Arg Ala Arg Thr Cys Ala Pro Cys Val
        610   615   620

atc ttc ttt gat gag gtg gat gct ttg aca aca agt cgt ggc aaa gaa   1920
Ile Phe Phe Asp Glu Val Asp Ala Leu Thr Thr Ser Arg Gly Lys Glu
625   630   635   640

ggt gct tgg gtt gtt gaa cgg ctt ttg aac cag ttt ctt gtt gag ctg   1968
Gly Ala Trp Val Val Glu Arg Leu Leu Asn Gln Phe Leu Val Glu Leu
                645   650   655

gat ggt gga gag agg cgt aat gta tat gta att gga gct aca aac agg   2016
Asp Gly Gly Glu Arg Arg Asn Val Tyr Val Ile Gly Ala Thr Asn Arg
                660   665   670

cca gat gta gtt gat cct gct ttc ttg aga ccg ggt aga ttt ggg aat   2064
Pro Asp Val Val Asp Pro Ala Phe Leu Arg Pro Gly Arg Phe Gly Asn
                675   680   685

ctt ctt tat gta ccc ctc ccc aac gca gat gag cgt gct tca att cta   2112
Leu Leu Tyr Val Pro Leu Pro Asn Ala Asp Glu Arg Ala Ser Ile Leu
        690   695   700

aaa gct att gca agg aag aaa ccg ata gat cct agt gtt gat ctg gat   2160
Lys Ala Ile Ala Arg Lys Lys Pro Ile Asp Pro Ser Val Asp Leu Asp
705   710   715   720

gga att gca aag aat aac tgt gaa ggt ttc agc gga gct gat ctc gca   2208
Gly Ile Ala Lys Asn Asn Cys Glu Gly Phe Ser Gly Ala Asp Leu Ala
                725   730   735

cac ttg gtg caa aaa gct aca ttc caa gca gtg gag gag atg ata ggc   2256
His Leu Val Gln Lys Ala Thr Phe Gln Ala Val Glu Glu Met Ile Gly
                740   745   750

tcc agt gag tcg tct gaa gat gat gtt aca gat ata acg cag tgt aca   2304
Ser Ser Glu Ser Ser Glu Asp Asp Val Thr Asp Ile Thr Gln Cys Thr
                755   760   765

atc aag acg agg cat ttc gag caa gcc ttg tcc tta gtc tca cca tct   2352
Ile Lys Thr Arg His Phe Glu Gln Ala Leu Ser Leu Val Ser Pro Ser
        770   775   780

gtg aac aaa cag caa aga aga cac tat gac gca cta tca aca aag ctt   2400

61

```
Val Asn Lys Gln Gln Arg Arg His Tyr Asp Ala Leu Ser Thr Lys Leu
785                 790             795                 800

caa gaa agc gtt ggg agg aac act gaa caa gtc acc ata ggg cca tct    2448
Gln Glu Ser Val Gly Arg Asn Thr Glu Gln Val Thr Ile Gly Pro Ser
                805             810                 815

ttt acc ctc gag taa                                                2463
Phe Thr Leu Glu
            820
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<210> 26

<211> 820

<212> PRT

<213> Arabidopsis thaliana

<400> 26

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Met Gly Arg Arg Gly Arg Gly Gly Gly Gly Met Gly Gly Gly Ile
1               5               10              15

Asn Arg Arg Tyr Leu Ser Gln Val Met Asp Thr Cys Gly Lys Asp Leu
            20              25              30

Ser Thr Ala Glu Asp Ile Val Asp Asp Leu Arg Ser Arg Tyr Gly Asn
        35              40              45

Phe Ala Arg Leu Thr Arg Gln Val Leu Leu Leu Asn Val Arg Gln Val
    50              55              60

Leu Asn Val Arg Asn Asn Lys Arg Val Lys Asp Glu Asp Glu Asp Asp
65              70              75              80

Asn Ile Gly Asp Glu Glu Gly Ser Ala Ser Gln Arg Lys Lys Gln Arg
            85              90              95

Arg Val Asp Glu Lys Glu Glu Lys Leu Gln Arg Ala Glu Gln Ser His
            100             105             110

Leu Arg Lys Arg Asn Met Glu Arg Ser Val Ser Ser Ser Pro Ser Ser
        115             120             125

Ser Ser Ser Ser Glu Asp Ser Gly Asp Val Ser Thr Ser Glu Asp Ala
    130             135             140
```

```
Val Tyr Gly Glu Lys Leu Ser Pro Pro Arg Phe Asp Leu Ile Asn Asp
145             150             155             160


Ser Leu Arg Asp Asn Tyr Ala Lys Leu Asn Ser Ser Ser Lys Lys Pro
                165             170             175


Ile Gly Ser Pro Ala Glu Lys Asn Val Glu Val Glu Thr Val Ser Asn
            180             185             190


Lys Gly Arg Ser Lys Leu Ala Thr Met Gly Ala Arg Lys Glu Ala Lys
        195             200             205


Val Ser Leu Ser Leu Ser Gly Ala Thr Gly Asn Gly Asp Leu Glu Val
    210             215             220


Glu Gly Thr Lys Gly Pro Thr Phe Lys Asp Phe Gly Gly Ile Lys Lys
225             230             235             240


Ile Leu Asp Glu Leu Glu Met Asn Val Leu Phe Pro Ile Leu Asn Pro
            245             250             255


Glu Pro Phe Lys Lys Ile Gly Val Lys Pro Pro Ser Gly Ile Leu Phe
            260             265             270


His Gly Pro Pro Gly Cys Gly Lys Thr Lys Leu Ala Asn Ala Ile Ala
        275             280             285


Asn Glu Ala Gly Val Pro Phe Tyr Lys Ile Ser Ala Thr Glu Val Ile
    290             295             300


Ser Gly Val Ser Gly Ala Ser Glu Glu Asn Ile Arg Glu Leu Phe Ser
305             310             315             320


Lys Ala Tyr Arg Thr Ala Pro Ser Ile Val Phe Ile Asp Glu Ile Asp
            325             330             335


Ala Ile Gly Ser Lys Arg Glu Asn Gln Gln Arg Glu Met Glu Lys Arg
            340             345             350


Ile Val Thr Gln Leu Leu Thr Cys Met Asp Gly Pro Gly Asn Lys Gly
        355             360             365


Asp Lys Asn Ala Pro Asp Ser Ser Ala Gly Phe Val Leu Val Ile Gly
        370             375             380
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Ala Thr Asn Arg Pro Asp Ala Leu Asp Pro Ala Leu Arg Arg Ser Gly
385   390   395   400

Arg Phe Glu Thr Glu Ile Ala Leu Thr Ala Pro Asp Glu Asp Ala Arg
                405   410   415

Ala Glu Ile Leu Ser Val Val Ala Gln Lys Leu Arg Leu Glu Gly Pro
                420   425   430

Phe Asp Lys Lys Arg Ile Ala Arg Leu Thr Pro Gly Phe Val Gly Ala
        435   440   445

Asp Leu Glu Ser Val Ala Tyr Leu Ala Gly Arg Lys Ala Ile Lys Arg
        450   455   460

Ile Leu Asp Ser Arg Lys Ser Glu Gln Ser Gly Asp Gly Glu Asp Asp
465   470   475   480

Lys Ser Trp Leu Arg Met Pro Trp Pro Glu Glu Glu Leu Glu Lys Leu
            485   490   495

Phe Val Lys Met Ser Asp Phe Glu Glu Ala Val Asn Leu Val Gln Ala
            500   505   510

Ser Leu Thr Arg Glu Gly Phe Ser Ile Val Pro Asp Val Lys Trp Asp
        515   520   525

Asp Val Gly Gly Leu Asp His Leu Arg Leu Gln Phe Asn Arg Tyr Ile
        530   535   540

Val Arg Pro Ile Lys Lys Pro Asp Ile Tyr Lys Ala Phe Gly Val Asp
545   550   555   560

Leu Glu Thr Gly Phe Leu Leu Tyr Gly Pro Pro Gly Cys Gly Lys Thr
            565   570   575

Leu Ile Ala Lys Ala Ala Ala Asn Glu Ala Gly Ala Asn Phe Met His
            580   585   590

Ile Lys Gly Ala Glu Leu Leu Asn Lys Tyr Val Gly Glu Ser Glu Leu
        595   600   605

Ala Ile Arg Thr Leu Phe Gln Arg Ala Arg Thr Cys Ala Pro Cys Val
610   615   620

64

Ile Phe Phe Asp Glu Val Asp Ala Leu Thr Thr Ser Arg Gly Lys Glu
625   630   635   640

Gly Ala Trp Val Val Glu Arg Leu Leu Asn Gln Phe Leu Val Glu Leu
                    645   650   655

Asp Gly Gly Glu Arg Arg Asn Val Tyr Val Ile Gly Ala Thr Asn Arg
                660   665   670

Pro Asp Val Val Asp Pro Ala Phe Leu Arg Pro Gly Arg Phe Gly Asn
            675   680   685

Leu Leu Tyr Val Pro Leu Pro Asn Ala Asp Glu Arg Ala Ser Ile Leu
    690   695   700

Lys Ala Ile Ala Arg Lys Lys Pro Ile Asp Pro Ser Val Asp Leu Asp
705   710   715   720

Gly Ile Ala Lys Asn Asn Cys Glu Gly Phe Ser Gly Ala Asp Leu Ala
                725   730   735

His Leu Val Gln Lys Ala Thr Phe Gln Ala Val Glu Glu Met Ile Gly
            740   745   750

Ser Ser Glu Ser Ser Glu Asp Asp Val Thr Asp Ile Thr Gln Cys Thr
        755   760   765

Ile Lys Thr Arg His Phe Glu Gln Ala Leu Ser Leu Val Ser Pro Ser
    770   775   780

Val Asn Lys Gln Gln Arg Arg His Tyr Asp Ala Leu Ser Thr Lys Leu
785   790   795   800

Gln Glu Ser Val Gly Arg Asn Thr Glu Gln Val Thr Ile Gly Pro Ser
                805   810   815

Phe Thr Leu Glu
            820

<210> 27

<211> 1002

<212> DNA

<213> Arabidopsis thaliana

65

<220>

<221>   CDS

<222>   (1)..(1002)

<223>   14891

<400>   27

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atg gag gtg aca aat acg agc agc atc atg tgg ttc ttc agg gac aaa        48
Met Glu Val Thr Asn Thr Ser Ser Ile Met Trp Phe Phe Arg Asp Lys
1               5                   10                  15

ggt ttc gat gat ccg agt atc gac aag atg ttg aga aaa tgc aaa cag        96
Gly Phe Asp Asp Pro Ser Ile Asp Lys Met Leu Arg Lys Cys Lys Gln
                20                  25                  30

ttg gaa aag gct caa agc gat gtg gca tca gaa aac tgg gac tac ctg       144
Leu Glu Lys Ala Gln Ser Asp Val Ala Ser Glu Asn Trp Asp Tyr Leu
            35                  40                  45

agt aac att gtt ggt atc caa gag aga aaa ctc cct tac atc gtc tct       192
Ser Asn Ile Val Gly Ile Gln Glu Arg Lys Leu Pro Tyr Ile Val Ser
        50                  55                  60

cga tgc ccc aaa atc ctg act tta cgc ctc gat gag aga ctc atc ccg       240
Arg Cys Pro Lys Ile Leu Thr Leu Arg Leu Asp Glu Arg Leu Ile Pro
65                  70                  75                  80

atg gtc gag tgc ctc tcc agt ctt gga agg aat cct cgg gaa gtt gct       288
Met Val Glu Cys Leu Ser Ser Leu Gly Arg Asn Pro Arg Glu Val Ala
                85                  90                  95

tcc gcc att acc aaa ttt cct cca ata ctc tct cat agc gtg gag gag       336
Ser Ala Ile Thr Lys Phe Pro Pro Ile Leu Ser His Ser Val Glu Glu
                100                 105                 110

aaa ctc tgt ccc ctt ctt gct ttc ttt caa gcg tta ggt gtg cct gag       384
Lys Leu Cys Pro Leu Leu Ala Phe Phe Gln Ala Leu Gly Val Pro Glu
            115                 120                 125

act caa ctt ggc aaa atg ata ctt ttt aac cca agg ctt atc agc tac       432
Thr Gln Leu Gly Lys Met Ile Leu Phe Asn Pro Arg Leu Ile Ser Tyr
        130                 135                 140

agc atc gac acc aag ctg aca gtg atc gtc agc ttt ctt gct agc ctt       480
Ser Ile Asp Thr Lys Leu Thr Val Ile Val Ser Phe Leu Ala Ser Leu
145                 150                 155                 160

ggc ctt gat caa gat ggg atg att ggc aaa gtt ttg gtg aag aac cca       528
Gly Leu Asp Gln Asp Gly Met Ile Gly Lys Val Leu Val Lys Asn Pro
                165                 170                 175

ttt ctt atg ggg tac agt gtt gat aaa agg tta cgg cct acc act gaa       576
Phe Leu Met Gly Tyr Ser Val Asp Lys Arg Leu Arg Pro Thr Thr Glu
                180                 185                 190
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66

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ttc ttg aaa tca tcc gtt ggc ctg agt gag gat ggc att aag tcg gtg     624
Phe Leu Lys Ser Ser Val Gly Leu Ser Glu Asp Gly Ile Lys Ser Val
        195                 200                 205

gtc atg aat ttc cca caa ctt ttg tgc aga gac gtt aac aag att ctc     672
Val Met Asn Phe Pro Gln Leu Leu Cys Arg Asp Val Asn Lys Ile Leu
    210                 215                 220

aaa cca aat tat gat tat ttg aag gag tgt ggg ttt gga gat tcc cag     720
Lys Pro Asn Tyr Asp Tyr Leu Lys Glu Cys Gly Phe Gly Asp Ser Gln
225                 230                 235                 240

ata gca acc atg gtc act ggt tat ccc caa atc ttg att aag agt gtt     768
Ile Ala Thr Met Val Thr Gly Tyr Pro Gln Ile Leu Ile Lys Ser Val
                245                 250                 255

aag aat tca cta cag cct agg atc aga ttc ctc gtc cag gtg atg gga     816
Lys Asn Ser Leu Gln Pro Arg Ile Arg Phe Leu Val Gln Val Met Gly
            260                 265                 270

aga ggc atg gat gaa gtg gct tct tat cct gaa ttc ttt cac cat gga     864
Arg Gly Met Asp Glu Val Ala Ser Tyr Pro Glu Phe Phe His His Gly
            275                 280                 285

ttg aag aag aag gtc gaa tcg agg ttt aaa ctt gtc aaa aag aac aac     912
Leu Lys Lys Lys Val Glu Ser Arg Phe Lys Leu Val Lys Lys Asn Asn
        290                 295                 300

att gac tgc agc ctt aga gaa atg ctg gac tgt aac aca aag aaa ttc     960
Ile Asp Cys Ser Leu Arg Glu Met Leu Asp Cys Asn Thr Lys Lys Phe
305                 310                 315                 320

cat gag aag ttt ggc ttt tcg gag gta act gca agc tcc tag           1002
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<210> 28

<211> 333

<212> PRT

<213> Arabidopsis thaliana

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1               5                   10                  15


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                20                  25                  30


Leu Glu Lys Ala Gln Ser Asp Val Ala Ser Glu Asn Trp Asp Tyr Leu
            35                  40                  45
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67

Ser Asn Ile Val Gly Ile Gln Glu Arg Lys Leu Pro Tyr Ile Val Ser
50   55   60

Arg Cys Pro Lys Ile Leu Thr Leu Arg Leu Asp Glu Arg Leu Ile Pro
65   70   75   80

Met Val Glu Cys Leu Ser Ser Leu Gly Arg Asn Pro Arg Glu Val Ala
85   90   95

Ser Ala Ile Thr Lys Phe Pro Pro Ile Leu Ser His Ser Val Glu Glu
100   105   110

Lys Leu Cys Pro Leu Leu Ala Phe Phe Gln Ala Leu Gly Val Pro Glu
115   120   125

Thr Gln Leu Gly Lys Met Ile Leu Phe Asn Pro Arg Leu Ile Ser Tyr
130   135   140

Ser Ile Asp Thr Lys Leu Thr Val Ile Val Ser Phe Leu Ala Ser Leu
145   150   155   160

Gly Leu Asp Gln Asp Gly Met Ile Gly Lys Val Leu Val Lys Asn Pro
165   170   175

Phe Leu Met Gly Tyr Ser Val Asp Lys Arg Leu Arg Pro Thr Thr Glu
180   185   190

Phe Leu Lys Ser Ser Val Gly Leu Ser Glu Asp Gly Ile Lys Ser Val
195   200   205

Val Met Asn Phe Pro Gln Leu Leu Cys Arg Asp Val Asn Lys Ile Leu
210   215   220

Lys Pro Asn Tyr Asp Tyr Leu Lys Glu Cys Gly Phe Gly Asp Ser Gln
225   230   235   240

Ile Ala Thr Met Val Thr Gly Tyr Pro Gln Ile Leu Ile Lys Ser Val
245   250   255

Lys Asn Ser Leu Gln Pro Arg Ile Arg Phe Leu Val Gln Val Met Gly
260   265   270

Arg Gly Met Asp Glu Val Ala Ser Tyr Pro Glu Phe Phe His His Gly
275   280   285

68

Leu Lys Lys Lys Val Glu Ser Arg Phe Lys Leu Val Lys Lys Asn Asn
    290   295   300

Ile Asp Cys Ser Leu Arg Glu Met Leu Asp Cys Asn Thr Lys Lys Phe
305   310   315   320

His Glu Lys Phe Gly Phe Ser Glu Val Thr Ala Ser Ser
            325   330

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<211>   2394

<212>   DNA

<213>   Arabidopsis thaliana

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<223>   14986

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Met Glu Leu Leu Arg Ser Asn Leu Ser Arg Val Gln Ile Pro Glu Pro
1   5   10   15

act cat cgc atc tac aag cat gag tgt tgc atc tcc ttc gat act ccg   96
Thr His Arg Ile Tyr Lys His Glu Cys Cys Ile Ser Phe Asp Thr Pro
                20   25   30

aga tcc gaa gga gga ttg ttc gtt gat atg aat agt ttt ctt gct ttc   144
Arg Ser Glu Gly Gly Leu Phe Val Asp Met Asn Ser Phe Leu Ala Phe
            35   40   45

ggg aag gat tat gtt tct tgg aac tat gag aag act gga aac cct gtt   192
Gly Lys Asp Tyr Val Ser Trp Asn Tyr Glu Lys Thr Gly Asn Pro Val
    50   55   60

tat ctt cat att aag cag act agg aag tct att ccc gag gat cgg cct   240
Tyr Leu His Ile Lys Gln Thr Arg Lys Ser Ile Pro Glu Asp Arg Pro
65   70   75   80

ctc aag aaa ccg act ctg ctc gct ata ggt gtt gat gga ggc ttt gat   288
Leu Lys Lys Pro Thr Leu Leu Ala Ile Gly Val Asp Gly Gly Phe Asp
                85   90   95

aac aat gag cca gag tac gag gag tct tat agc ata gtc ata ctt ccg   336

69

```
Asn Asn Glu Pro Glu Tyr Glu Glu Ser Tyr Ser Ile Val Ile Leu Pro
            100                 105                 110

gat ttt gtt tca ctc ccg ttt cct tct gtt gag cta cca gag aag gtg        384
Asp Phe Val Ser Leu Pro Phe Pro Ser Val Glu Leu Pro Glu Lys Val
            115                 120                 125

agg att gct gtc gat act gta gtg aat gcc gtt ggt gct gag cgg aaa        432
Arg Ile Ala Val Asp Thr Val Val Asn Ala Val Gly Ala Glu Arg Lys
    130                 135                 140

gag caa gtt gca gct tgg aca gct gag aaa aag tta att agt gaa cat        480
Glu Gln Val Ala Ala Trp Thr Ala Glu Lys Lys Leu Ile Ser Glu His
145                 150                 155                 160

gca ttg aca ctg cag caa atc aag agt ggc att gtc att cct ccc tct        528
Ala Leu Thr Leu Gln Gln Ile Lys Ser Gly Ile Val Ile Pro Pro Ser
                165                 170                 175

ggt tgg aaa tgt tct aag tgt gat aag acg gag aat ctc tgg ctt aat        576
Gly Trp Lys Cys Ser Lys Cys Asp Lys Thr Glu Asn Leu Trp Leu Asn
                180                 185                 190

ctt acc gat gga atg att ctc tgt gga aga aaa aac tgg gat gga act        624
Leu Thr Asp Gly Met Ile Leu Cys Gly Arg Lys Asn Trp Asp Gly Thr
            195                 200                 205

ggt gga aac aac cat gct gtt gag cac tac aaa gag aca gcc tac cct        672
Gly Gly Asn Asn His Ala Val Glu His Tyr Lys Glu Thr Ala Tyr Pro
    210                 215                 220

ctt gct gta aag ctt gga act atc act gct gac tta gaa gca gca gat        720
Leu Ala Val Lys Leu Gly Thr Ile Thr Ala Asp Leu Glu Ala Ala Asp
225                 230                 235                 240

gtt tat tcc tat ccg gaa gat gac agt gtt ttg gac ccg ctc ctg gct        768
Val Tyr Ser Tyr Pro Glu Asp Asp Ser Val Leu Asp Pro Leu Leu Ala
                245                 250                 255

gag cat ctg gcc cat ttt gga att gac ttc tcg tcg atg cag aag act        816
Glu His Leu Ala His Phe Gly Ile Asp Phe Ser Ser Met Gln Lys Thr
                260                 265                 270

gaa atg aca act gct gaa aga gaa ctt gat caa aat aca aat ttt gat        864
Glu Met Thr Thr Ala Glu Arg Glu Leu Asp Gln Asn Thr Asn Phe Asp
            275                 280                 285

tgg aac cgt ata caa gag agt gga aaa gaa ttg gtg cca gtt ttt gga        912
Trp Asn Arg Ile Gln Glu Ser Gly Lys Glu Leu Val Pro Val Phe Gly
    290                 295                 300

cct gga tat acc gga ctt gtc aat ctt ggg aac agt tgc tac ttg gca        960
Pro Gly Tyr Thr Gly Leu Val Asn Leu Gly Asn Ser Cys Tyr Leu Ala
305                 310                 315                 320

gct acg atg cag att gtt ttc tct acc cat tca ttt att tca aga tac       1008
Ala Thr Met Gln Ile Val Phe Ser Thr His Ser Phe Ile Ser Arg Tyr
                325                 330                 335

ttt tca cat cag agc tta aag atg gct ttt gag atg gct cct gct gat       1056
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70

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Phe Ser His Gln Ser Leu Lys Met Ala Phe Glu Met Ala Pro Ala Asp
        340             345             350

cca act ttg gac ctc aat atg caa tta aca aag ctt gga cac ggc tta    1104
Pro Thr Leu Asp Leu Asn Met Gln Leu Thr Lys Leu Gly His Gly Leu
        355             360             365

cta tct ggg aag tac tca atg cct gca act cag aag gat gct aca act    1152
Leu Ser Gly Lys Tyr Ser Met Pro Ala Thr Gln Lys Asp Ala Thr Thr
        370             375             380

gga gat cct aga caa gaa gga ata cct cct cgc atg ttc aaa aac gta    1200
Gly Asp Pro Arg Gln Glu Gly Ile Pro Pro Arg Met Phe Lys Asn Val
385             390             395             400

att gcc gcg agc cac gca gaa ttc tct tct atg aga cag cag gat gct    1248
Ile Ala Ala Ser His Ala Glu Phe Ser Ser Met Arg Gln Gln Asp Ala
            405             410             415

ctc gac ttt ttc ctc cat ctg gta ggc aag gtt gag cgt gct agc aac    1296
Leu Asp Phe Phe Leu His Leu Val Gly Lys Val Glu Arg Ala Ser Asn
        420             425             430

acg aca cca gat tta gac ccc tcg agg agc ttc aag ttt gga ata gaa    1344
Thr Thr Pro Asp Leu Asp Pro Ser Arg Ser Phe Lys Phe Gly Ile Glu
        435             440             445

gag aag atc ctt tgt ccg tct gga aag gtt gga tat aat aag agg gaa    1392
Glu Lys Ile Leu Cys Pro Ser Gly Lys Val Gly Tyr Asn Lys Arg Glu
        450             455             460

gac tgt att ctt tct ttg aac att ccg cta cat gag gca act aat aaa    1440
Asp Cys Ile Leu Ser Leu Asn Ile Pro Leu His Glu Ala Thr Asn Lys
465             470             475             480

gat gaa tta gaa gcc ttt cac aag caa aaa gca gga aaa gga ttg gaa    1488
Asp Glu Leu Glu Ala Phe His Lys Gln Lys Ala Gly Lys Gly Leu Glu
            485             490             495

gag aat gat atg agg tca agt gat gaa ata gta cgc cca cga gtt cct    1536
Glu Asn Asp Met Arg Ser Ser Asp Glu Ile Val Arg Pro Arg Val Pro
        500             505             510

tta gaa gcc tgt cta gca aat ttt gca tca tca gag ccg att gaa gac    1584
Leu Glu Ala Cys Leu Ala Asn Phe Ala Ser Ser Glu Pro Ile Glu Asp
        515             520             525

tac tat agc tct gct ttg aag gga atg aca aca gct atc aag aca act    1632
Tyr Tyr Ser Ser Ala Leu Lys Gly Met Thr Thr Ala Ile Lys Thr Thr
        530             535             540

ggt ttg aca tct ttc cca gat tat ttg gtc ttg cac atg cgg aaa ttt    1680
Gly Leu Thr Ser Phe Pro Asp Tyr Leu Val Leu His Met Arg Lys Phe
545             550             555             560

gtt atg gag gaa ggc tgg gtg cca aag aaa ctt gat gta tac att gat    1728
Val Met Glu Glu Gly Trp Val Pro Lys Lys Leu Asp Val Tyr Ile Asp
                565             570             575

gtt ccg gat gtt att gat atc agc cac atg cgt agc aaa gga ctc caa    1776
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    Val Pro Asp Val Ile Asp Ile Ser His Met Arg Ser Lys Gly Leu Gln
            580             585             590

cct ggg gaa gaa ctg ttg cca gat ggc gtt cca gaa gaa gtg atg gaa      1824
Pro Gly Glu Glu Leu Leu Pro Asp Gly Val Pro Glu Glu Val Met Glu
        595             600             605

tca gcg cag ccc gtg gca aat gag gag ata gtt gca cag cta gtc tca      1872
Ser Ala Gln Pro Val Ala Asn Glu Glu Ile Val Ala Gln Leu Val Ser
    610             615             620

atg gga ttt agc cag ctt cac tgc cag aaa gct gcc ata aat act tcc      1920
Met Gly Phe Ser Gln Leu His Cys Gln Lys Ala Ala Ile Asn Thr Ser
625             630             635             640

aat gct ggg gtt gaa gag gca atg aac tgg tta ctt tct cac atg gat      1968
Asn Ala Gly Val Glu Glu Ala Met Asn Trp Leu Leu Ser His Met Asp
            645             650             655

gat cca gac atc gat gca cca atc tcc cac cag aca tct gac att gat      2016
Asp Pro Asp Ile Asp Ala Pro Ile Ser His Gln Thr Ser Asp Ile Asp
            660             665             670

caa tca agc gtt gat acc tta ctc tcc ttt ggt ttt gct gaa gat gtt      2064
Gln Ser Ser Val Asp Thr Leu Leu Ser Phe Gly Phe Ala Glu Asp Val
    675             680             685

gct cgg aag gca cta aaa gcc tcg gga gga gac att gag aaa gca aca      2112
Ala Arg Lys Ala Leu Lys Ala Ser Gly Gly Asp Ile Glu Lys Ala Thr
    690             695             700

gac tgg gta ttc aac aac cct aat gca tct gtt tca gac atg gat gta      2160
Asp Trp Val Phe Asn Asn Pro Asn Ala Ser Val Ser Asp Met Asp Val
705             710             715             720

tcc tct agc aat tca gcg cag act ccg gct caa agt gga tta cca gat      2208
Ser Ser Ser Asn Ser Ala Gln Thr Pro Ala Gln Ser Gly Leu Pro Asp
            725             730             735

gga gga ggg aaa tac aag ctg ttt gga ata gta agt cac atg gga aca      2256
Gly Gly Gly Lys Tyr Lys Leu Phe Gly Ile Val Ser His Met Gly Thr
            740             745             750

tca gtg cac tgt ggt cat tac gtg gct cac ata ttg aaa gaa ggc cgc      2304
Ser Val His Cys Gly His Tyr Val Ala His Ile Leu Lys Glu Gly Arg
            755             760             765

tgg gta att ttc aat gac gac aaa gtt ggt atc tcg act gat cct cct      2352
Trp Val Ile Phe Asn Asp Asp Lys Val Gly Ile Ser Thr Asp Pro Pro
770             775             780

aaa gac atg ggt tat gtc tac ttc ttt cag cgg ctt gat tga            2394
Lys Asp Met Gly Tyr Val Tyr Phe Phe Gln Arg Leu Asp
785             790             795
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<211>   797

72

<212>   PRT

<213>   Arabidopsis thaliana

<400>   30

Met Glu Leu Leu Arg Ser Asn Leu Ser Arg Val Gln Ile Pro Glu Pro
1   5   10   15

Thr His Arg Ile Tyr Lys His Glu Cys Cys Ile Ser Phe Asp Thr Pro
                20   25   30

Arg Ser Glu Gly Gly Leu Phe Val Asp Met Asn Ser Phe Leu Ala Phe
            35   40   45

Gly Lys Asp Tyr Val Ser Trp Asn Tyr Glu Lys Thr Gly Asn Pro Val
        50   55   60

Tyr Leu His Ile Lys Gln Thr Arg Lys Ser Ile Pro Glu Asp Arg Pro
65   70   75   80

Leu Lys Lys Pro Thr Leu Leu Ala Ile Gly Val Asp Gly Gly Phe Asp
                85   90   95

Asn Asn Glu Pro Glu Tyr Glu Glu Ser Tyr Ser Ile Val Ile Leu Pro
                100   105   110

Asp Phe Val Ser Leu Pro Phe Pro Ser Val Glu Leu Pro Glu Lys Val
            115   120   125

Arg Ile Ala Val Asp Thr Val Val Asn Ala Val Gly Ala Glu Arg Lys
        130   135   140

Glu Gln Val Ala Ala Trp Thr Ala Glu Lys Lys Leu Ile Ser Glu His
145   150   155   160

Ala Leu Thr Leu Gln Gln Ile Lys Ser Gly Ile Val Ile Pro Pro Ser
                165   170   175

Gly Trp Lys Cys Ser Lys Cys Asp Lys Thr Glu Asn Leu Trp Leu Asn
            180   185   190

Leu Thr Asp Gly Met Ile Leu Cys Gly Arg Lys Asn Trp Asp Gly Thr
            195   200   205

73

Gly Gly Asn Asn His Ala Val Glu His Tyr Lys Glu Thr Ala Tyr Pro
    210   215   220

Leu Ala Val Lys Leu Gly Thr Ile Thr Ala Asp Leu Glu Ala Ala Asp
225   230   235   240

Val Tyr Ser Tyr Pro Glu Asp Asp Ser Val Leu Asp Pro Leu Leu Ala
                245   250   255

Glu His Leu Ala His Phe Gly Ile Asp Phe Ser Ser Met Gln Lys Thr
            260   265   270

Glu Met Thr Thr Ala Glu Arg Glu Leu Asp Gln Asn Thr Asn Phe Asp
        275   280   285

Trp Asn Arg Ile Gln Glu Ser Gly Lys Glu Leu Val Pro Val Phe Gly
    290   295   300

Pro Gly Tyr Thr Gly Leu Val Asn Leu Gly Asn Ser Cys Tyr Leu Ala
305   310   315   320

Ala Thr Met Gln Ile Val Phe Ser Thr His Ser Phe Ile Ser Arg Tyr
            325   330   335

Phe Ser His Gln Ser Leu Lys Met Ala Phe Glu Met Ala Pro Ala Asp
            340   345   350

Pro Thr Leu Asp Leu Asn Met Gln Leu Thr Lys Leu Gly His Gly Leu
        355   360   365

Leu Ser Gly Lys Tyr Ser Met Pro Ala Thr Gln Lys Asp Ala Thr Thr
    370   375   380

Gly Asp Pro Arg Gln Glu Gly Ile Pro Pro Arg Met Phe Lys Asn Val
385   390   395   400

Ile Ala Ala Ser His Ala Glu Phe Ser Ser Met Arg Gln Gln Asp Ala
            405   410   415

Leu Asp Phe Phe Leu His Leu Val Gly Lys Val Glu Arg Ala Ser Asn
        420   425   430

Thr Thr Pro Asp Leu Asp Pro Ser Arg Ser Phe Lys Phe Gly Ile Glu
        435   440   445

74

Glu Lys Ile Leu Cys Pro Ser Gly Lys Val Gly Tyr Asn Lys Arg Glu
    450   455   460

Asp Cys Ile Leu Ser Leu Asn Ile Pro Leu His Glu Ala Thr Asn Lys
465   470   475   480

Asp Glu Leu Glu Ala Phe His Lys Gln Lys Ala Gly Lys Gly Leu Glu
            485   490   495

Glu Asn Asp Met Arg Ser Ser Asp Glu Ile Val Arg Pro Arg Val Pro
            500   505   510

Leu Glu Ala Cys Leu Ala Asn Phe Ala Ser Ser Glu Pro Ile Glu Asp
            515   520   525

Tyr Tyr Ser Ser Ala Leu Lys Gly Met Thr Thr Ala Ile Lys Thr Thr
    530   535   540

Gly Leu Thr Ser Phe Pro Asp Tyr Leu Val Leu His Met Arg Lys Phe
545   550   555   560

Val Met Glu Glu Gly Trp Val Pro Lys Lys Leu Asp Val Tyr Ile Asp
            565   570   575

Val Pro Asp Val Ile Asp Ile Ser His Met Arg Ser Lys Gly Leu Gln
            580   585   590

Pro Gly Glu Glu Leu Leu Pro Asp Gly Val Pro Glu Glu Val Met Glu
    595   600   605

Ser Ala Gln Pro Val Ala Asn Glu Glu Ile Val Ala Gln Leu Val Ser
    610   615   620

Met Gly Phe Ser Gln Leu His Cys Gln Lys Ala Ala Ile Asn Thr Ser
625   630   635   640

Asn Ala Gly Val Glu Glu Ala Met Asn Trp Leu Leu Ser His Met Asp
            645   650   655

Asp Pro Asp Ile Asp Ala Pro Ile Ser His Gln Thr Ser Asp Ile Asp
            660   665   670

Gln Ser Ser Val Asp Thr Leu Leu Ser Phe Gly Phe Ala Glu Asp Val
    675   680   685

75

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Ala Arg Lys Ala Leu Lys Ala Ser Gly Gly Asp Ile Glu Lys Ala Thr
    690             695             700

Asp Trp Val Phe Asn Asn Pro Asn Ala Ser Val Ser Asp Met Asp Val
705             710             715             720

Ser Ser Ser Asn Ser Ala Gln Thr Pro Ala Gln Ser Gly Leu Pro Asp
                725             730             735

Gly Gly Gly Lys Tyr Lys Leu Phe Gly Ile Val Ser His Met Gly Thr
            740             745             750

Ser Val His Cys Gly His Tyr Val Ala His Ile Leu Lys Glu Gly Arg
        755             760             765

Trp Val Ile Phe Asn Asp Asp Lys Val Gly Ile Ser Thr Asp Pro Pro
    770             775             780

Lys Asp Met Gly Tyr Val Tyr Phe Phe Gln Arg Leu Asp
785             790             795
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<210> 31

<211> 1068

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1068)

<223> 15377


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atg ata cta cgt cgt ttc atc tgc tac aac gct tct tca act gtt tca      48
Met Ile Leu Arg Arg Phe Ile Cys Tyr Asn Ala Ser Ser Thr Val Ser
1               5               10              15

tct ata gct cca tca ccg aag aag aag cct ctc atc ttc tta ggc tct      96
Ser Ile Ala Pro Ser Pro Lys Lys Lys Pro Leu Ile Phe Leu Gly Ser
            20              25              30

cct cag gtc tcc gtg agt gtg ctt gaa gct ctt ttc aat gca tct aat     144
Pro Gln Val Ser Val Ser Val Leu Glu Ala Leu Phe Asn Ala Ser Asn
        35              40              45
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76

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gct cca aac tct tcc ttc gag gtt gca ggt att gtt aca cag cct cca    192
Ala Pro Asn Ser Ser Phe Glu Val Ala Gly Ile Val Thr Gln Pro Pro
    50              55                  60

tca agg aga gat agg ggt aaa aaa gtg ttg cct tca cca gta gcg caa    240
Ser Arg Arg Asp Arg Gly Lys Lys Val Leu Pro Ser Pro Val Ala Gln
65              70                  75                  80

tac gct ctt gat aaa ggc tta cct tct gat ctc att ttc tcc cct gag    288
Tyr Ala Leu Asp Lys Gly Leu Pro Ser Asp Leu Ile Phe Ser Pro Glu
                85                  90                  95

aag gca gga gat gaa gca ttt tta tcg gct tta aga gag ttg caa cct    336
Lys Ala Gly Asp Glu Ala Phe Leu Ser Ala Leu Arg Glu Leu Gln Pro
                100                 105                 110

gag ctt tgt att aca gca gct tat ggg aat att ttg cct act aag ttc    384
Glu Leu Cys Ile Thr Ala Ala Tyr Gly Asn Ile Leu Pro Thr Lys Phe
            115                 120                 125

ctt aag att ccg gta cat ggg aca gtg aac ata cac cca agt ttg ctg    432
Leu Lys Ile Pro Val His Gly Thr Val Asn Ile His Pro Ser Leu Leu
        130                 135                 140

ccg ctg tac cgt ggt gca gct cca gtt caa aga gca tta cag gat ggt    480
Pro Leu Tyr Arg Gly Ala Ala Pro Val Gln Arg Ala Leu Gln Asp Gly
145                 150                 155                 160

gtc ccg gaa aca gga gta tca tta gca ttt act gtg cgt aag tta gat    528
Val Pro Glu Thr Gly Val Ser Leu Ala Phe Thr Val Arg Lys Leu Asp
                165                 170                 175

gca ggg cca gtg att gcc tct aag agg ttc caa gtg gat gat cta ata    576
Ala Gly Pro Val Ile Ala Ser Lys Arg Phe Gln Val Asp Asp Leu Ile
                180                 185                 190

aag gca cca gaa cta ctc tcg ttc cta ttt tct gaa ggt tct aat ctt    624
Lys Ala Pro Glu Leu Leu Ser Phe Leu Phe Ser Glu Gly Ser Asn Leu
                195                 200                 205

ctt atc cgt gaa ctt ccc tcg ata ttt gat ggg tcc gca aaa tca aaa    672
Leu Ile Arg Glu Leu Pro Ser Ile Phe Asp Gly Ser Ala Lys Ser Lys
        210                 215                 220

gca gct ccc caa gat gat tct aaa gct acc tta gct cca aag ata gct    720
Ala Ala Pro Gln Asp Asp Ser Lys Ala Thr Leu Ala Pro Lys Ile Ala
225                 230                 235                 240

cca gat gag gct tgg ctc tct ttt gac cag gaa gct ttt gtt cta cat    768
Pro Asp Glu Ala Trp Leu Ser Phe Asp Gln Glu Ala Phe Val Leu His
                245                 250                 255

aac aag gtt cgt gca ttt gca gga tgg ccg gga aca cga gca aaa gtt    816
Asn Lys Val Arg Ala Phe Ala Gly Trp Pro Gly Thr Arg Ala Lys Val
                260                 265                 270

gta gtc ctt gat gag aaa agc ggt cag caa aat gtg cta gag ctt aaa    864
Val Val Leu Asp Glu Lys Ser Gly Gln Gln Asn Val Leu Glu Leu Lys
        275                 280                 285
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77

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att atg tcc act cga gta tgc aaa gat ctg gaa att cag gat agt gaa          912
Ile Met Ser Thr Arg Val Cys Lys Asp Leu Glu Ile Gln Asp Ser Glu
    290             295             300

caa gat tat gta act ttc aag aaa ggt tca cta ata ttt ccc tgc aga          960
Gln Asp Tyr Val Thr Phe Lys Lys Gly Ser Leu Ile Phe Pro Cys Arg
305             310             315             320

gga ggt aca gct tta gag gta ctg gaa gtc cag ctt cct ggt aag aaa         1008
Gly Gly Thr Ala Leu Glu Val Leu Glu Val Gln Leu Pro Gly Lys Lys
                325             330             335

gcc atc aac gca gct gct ttt tgg aat ggc ttg aga ggt caa aag ctg         1056
Ala Ile Asn Ala Ala Ala Phe Trp Asn Gly Leu Arg Gly Gln Lys Leu
            340             345             350

aag aag cta tga                                                         1068
Lys Lys Leu
        355
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<210> 32

<211> 355

<212> PRT

<213> Arabidopsis thaliana

<400> 32

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Met Ile Leu Arg Arg Phe Ile Cys Tyr Asn Ala Ser Ser Thr Val Ser
1               5               10              15


Ser Ile Ala Pro Ser Pro Lys Lys Lys Pro Leu Ile Phe Leu Gly Ser
            20              25              30


Pro Gln Val Ser Val Ser Val Leu Glu Ala Leu Phe Asn Ala Ser Asn
            35              40              45


Ala Pro Asn Ser Ser Phe Glu Val Ala Gly Ile Val Thr Gln Pro Pro
    50              55              60


Ser Arg Arg Asp Arg Gly Lys Lys Val Leu Pro Ser Pro Val Ala Gln
65              70              75              80


Tyr Ala Leu Asp Lys Gly Leu Pro Ser Asp Leu Ile Phe Ser Pro Glu
                85              90              95


Lys Ala Gly Asp Glu Ala Phe Leu Ser Ala Leu Arg Glu Leu Gln Pro
            100             105             110
```

```
Glu Leu Cys Ile Thr Ala Ala Tyr Gly Asn Ile Leu Pro Thr Lys Phe
        115                 120                 125

Leu Lys Ile Pro Val His Gly Thr Val Asn Ile His Pro Ser Leu Leu
        130                 135                 140

Pro Leu Tyr Arg Gly Ala Ala Pro Val Gln Arg Ala Leu Gln Asp Gly
145             150                 155                     160

Val Pro Glu Thr Gly Val Ser Leu Ala Phe Thr Val Arg Lys Leu Asp
                165                 170                 175

Ala Gly Pro Val Ile Ala Ser Lys Arg Phe Gln Val Asp Asp Leu Ile
            180                 185                 190

Lys Ala Pro Glu Leu Leu Ser Phe Leu Phe Ser Glu Gly Ser Asn Leu
        195                 200                 205

Leu Ile Arg Glu Leu Pro Ser Ile Phe Asp Gly Ser Ala Lys Ser Lys
    210                 215                 220

Ala Ala Pro Gln Asp Asp Ser Lys Ala Thr Leu Ala Pro Lys Ile Ala
225             230                 235                     240

Pro Asp Glu Ala Trp Leu Ser Phe Asp Gln Glu Ala Phe Val Leu His
            245                 250                 255

Asn Lys Val Arg Ala Phe Ala Gly Trp Pro Gly Thr Arg Ala Lys Val
            260                 265                 270

Val Val Leu Asp Glu Lys Ser Gly Gln Gln Asn Val Leu Glu Leu Lys
        275                 280                 285

Ile Met Ser Thr Arg Val Cys Lys Asp Leu Glu Ile Gln Asp Ser Glu
    290                 295                 300

Gln Asp Tyr Val Thr Phe Lys Lys Gly Ser Leu Ile Phe Pro Cys Arg
305                 310                 315                 320

Gly Gly Thr Ala Leu Glu Val Leu Glu Val Gln Leu Pro Gly Lys Lys
                325                 330                 335

Ala Ile Asn Ala Ala Ala Phe Trp Asn Gly Leu Arg Gly Gln Lys Leu
            340                 345                 350
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79

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Lys Lys Leu
        355


<210>   33

<211>   2220

<212>   DNA

<213>   Arabidopsis thaliana


<220>

<221>   CDS

<222>   (1)..(2220)

<223>   16219


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atg ggt act tcg gtg caa gtg act cct ctc tgc gga gtt tac aac gag      48
Met Gly Thr Ser Val Gln Val Thr Pro Leu Cys Gly Val Tyr Asn Glu
1               5                   10                  15

aat cct ctc tcc tac tta gtc tcc att gat ggt ttc aac ttc ctc atc     96
Asn Pro Leu Ser Tyr Leu Val Ser Ile Asp Gly Phe Asn Phe Leu Ile
                20                  25                  30

gac tgt ggt tgg aac gat ctc ttc gac aca tcg ctc ctc gaa cct ctc    144
Asp Cys Gly Trp Asn Asp Leu Phe Asp Thr Ser Leu Leu Glu Pro Leu
            35                  40                  45

ccc agg gtt gct tct act ata gat gca gtt ttg ctt tct cat cca gat    192
Pro Arg Val Ala Ser Thr Ile Asp Ala Val Leu Leu Ser His Pro Asp
        50                  55                  60

aca ctt cac att ggt gct ctt cct tat gct atg aag cag ctt gga ctc    240
Thr Leu His Ile Gly Ala Leu Pro Tyr Ala Met Lys Gln Leu Gly Leu
65                  70                  75                  80

tcc gct cct gtt tat gct act gag cct gtt cat aga tta ggt ctc ctt    288
Ser Ala Pro Val Tyr Ala Thr Glu Pro Val His Arg Leu Gly Leu Leu
                85                  90                  95

aca atg tat gat cag ttt ttg tcc agg aag caa gta tcc gac ttt gat    336
Thr Met Tyr Asp Gln Phe Leu Ser Arg Lys Gln Val Ser Asp Phe Asp
                100                 105                 110

ctg ttt aca ctg gat gac ata gat tct gct ttc cag aat gtg atc aga    384
Leu Phe Thr Leu Asp Asp Ile Asp Ser Ala Phe Gln Asn Val Ile Arg
            115                 120                 125

ttg act tac tct caa aat tac cat ctt tct gga aag gga gag ggt att    432
```
                                        80

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Leu Thr Tyr Ser Gln Asn Tyr His Leu Ser Gly Lys Gly Glu Gly Ile
    130                 135                 140

gta att gct cct cat gtt gct gga cac atg ctg gga ggt agc atc tgg        480
Val Ile Ala Pro His Val Ala Gly His Met Leu Gly Gly Ser Ile Trp
145                 150                 155                 160

agg ata aca aag gat ggg gag gat gtt ata tat gct gtt gac tac aat        528
Arg Ile Thr Lys Asp Gly Glu Asp Val Ile Tyr Ala Val Asp Tyr Asn
                165                 170                 175

cat cgg aaa gaa agg cat ttg aat gga act gtt tta cag tct ttt gtt        576
His Arg Lys Glu Arg His Leu Asn Gly Thr Val Leu Gln Ser Phe Val
                180                 185                 190

cgg cct gct gtt ctg ata acc gat gca tat cat gct ctt tat acc aat        624
Arg Pro Ala Val Leu Ile Thr Asp Ala Tyr His Ala Leu Tyr Thr Asn
            195                 200                 205

caa acc gca aga cag caa agg gac aaa gaa ttt cta gat acc att tca        672
Gln Thr Ala Arg Gln Gln Arg Asp Lys Glu Phe Leu Asp Thr Ile Ser
        210                 215                 220

aaa cat ctt gaa gtt gga gga aat gtt cta ttg cca gta gac act gcg        720
Lys His Leu Glu Val Gly Gly Asn Val Leu Leu Pro Val Asp Thr Ala
225                 230                 235                 240

ggt cgt gtc ctg gaa ctt ctc ttg ata ctt gaa cag cat tgg tca caa        768
Gly Arg Val Leu Glu Leu Leu Leu Ile Leu Glu Gln His Trp Ser Gln
                245                 250                 255

aga ggt ttc agc ttt ccc att tat ttt ctc acg tac gtg tca tct agc        816
Arg Gly Phe Ser Phe Pro Ile Tyr Phe Leu Thr Tyr Val Ser Ser Ser
                260                 265                 270

aca att gac tat gtt aag agt ttc ctc gag tgg atg agt gac tcc att        864
Thr Ile Asp Tyr Val Lys Ser Phe Leu Glu Trp Met Ser Asp Ser Ile
            275                 280                 285

tca aag tcc ttt gag act tca cgt gat aat gcc ttt cta ttg agg cat        912
Ser Lys Ser Phe Glu Thr Ser Arg Asp Asn Ala Phe Leu Leu Arg His
        290                 295                 300

gtc act ctg ttg ata aac aag act gat ctg gat aat gct cca cct ggt        960
Val Thr Leu Leu Ile Asn Lys Thr Asp Leu Asp Asn Ala Pro Pro Gly
305                 310                 315                 320

cca aag gtt gtt ctt gct tcc atg gct agt ctc gaa gcc ggt ttt gct       1008
Pro Lys Val Val Leu Ala Ser Met Ala Ser Leu Glu Ala Gly Phe Ala
                325                 330                 335

cga gag ata ttc gtg gag tgg gca aat gat ccc aga aat tta gtc ctc       1056
Arg Glu Ile Phe Val Glu Trp Ala Asn Asp Pro Arg Asn Leu Val Leu
            340                 345                 350

ttt act gaa aca ggc cag ttt ggc act tta gct cgt atg ctt cag tca       1104
Phe Thr Glu Thr Gly Gln Phe Gly Thr Leu Ala Arg Met Leu Gln Ser
            355                 360                 365

gcc cca cct cca aaa ttt gtt aaa gtc acc atg tct aag agg gtt cct       1152
```

81

```
          Ala Pro Pro Pro Lys Phe Val Lys Val Thr Met Ser Lys Arg Val Pro
              370                 375                 380

          ttg gct ggg gaa gag tta att gca tat gag gaa gag caa aac aga ctg       1200
          Leu Ala Gly Glu Glu Leu Ile Ala Tyr Glu Glu Glu Gln Asn Arg Leu
          385                 390                 395                 400

          aaa agg gaa gaa gct ttg cga gct agc ctc gtt aaa gag gag gaa aca       1248
          Lys Arg Glu Glu Ala Leu Arg Ala Ser Leu Val Lys Glu Glu Glu Thr
                          405                 410                 415

          aaa gct tcc cat gga tcc gat gat aat tca agt gaa cct atg atc ata       1296
          Lys Ala Ser His Gly Ser Asp Asp Asn Ser Ser Glu Pro Met Ile Ile
                          420                 425                 430

          gat acc aag act act cac gat gtt gtt ggt tct cac ggg cct gca tat       1344
          Asp Thr Lys Thr Thr His Asp Val Val Gly Ser His Gly Pro Ala Tyr
                      435                 440                 445

          aaa gat ata ttg att gat gga ttt gtt ccc cca tcg agc agc gta gct       1392
          Lys Asp Ile Leu Ile Asp Gly Phe Val Pro Pro Ser Ser Ser Val Ala
              450                 455                 460

          cca atg ttc cca tat tat gat aac aca tct gaa tgg gac gac ttt ggg       1440
          Pro Met Phe Pro Tyr Tyr Asp Asn Thr Ser Glu Trp Asp Asp Phe Gly
          465                 470                 475                 480

          gag att att aat cca gat gac tat gtg atc aag gat gaa gac atg gac       1488
          Glu Ile Ile Asn Pro Asp Asp Tyr Val Ile Lys Asp Glu Asp Met Asp
                          485                 490                 495

          cga gga gca atg cat aac gga ggt gat gtg gac gga agg ctt gat gag       1536
          Arg Gly Ala Met His Asn Gly Gly Asp Val Asp Gly Arg Leu Asp Glu
                          500                 505                 510

          gca act gct agt ctc atg ctt gat aca aga cct tcg aaa gtc atg tcc       1584
          Ala Thr Ala Ser Leu Met Leu Asp Thr Arg Pro Ser Lys Val Met Ser
                      515                 520                 525

          aat gag ctc att gtg act gtt agt tgt tca ctt gtt aaa atg gac tat       1632
          Asn Glu Leu Ile Val Thr Val Ser Cys Ser Leu Val Lys Met Asp Tyr
          530                 535                 540

          gaa ggt cgg tca gat ggc cgc tca atc aag tca atg att gcg cat gtt       1680
          Glu Gly Arg Ser Asp Gly Arg Ser Ile Lys Ser Met Ile Ala His Val
          545                 550                 555                 560

          tct cct cta aaa ctt gtt ttg gtg cac gcg ata gct gag gct aca gag       1728
          Ser Pro Leu Lys Leu Val Leu Val His Ala Ile Ala Glu Ala Thr Glu
                          565                 570                 575

          cat ttg aag caa cac tgc ttg aac aac atc tgt cca cac gtg tat gct       1776
          His Leu Lys Gln His Cys Leu Asn Asn Ile Cys Pro His Val Tyr Ala
                          580                 585                 590

          cct caa ata gag gaa acg gtc gat gtg act tct gat tta tgt gct tac       1824
          Pro Gln Ile Glu Glu Thr Val Asp Val Thr Ser Asp Leu Cys Ala Tyr
                      595                 600                 605

          aag gtc caa ctt tct gaa aag ctg atg agc aat gtg atc ttc aag aag       1872
```

82

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Lys Val Gln Leu Ser Glu Lys Leu Met Ser Asn Val Ile Phe Lys Lys
    610             615             620

ctg gga gat tca gaa gta gct tgg gtg gat tcc gaa gta ggg aag aca    1920
Leu Gly Asp Ser Glu Val Ala Trp Val Asp Ser Glu Val Gly Lys Thr
625             630             635             640

gag agg gac atg agg tct cta cta ccg atg cca ggt gct gct tcg cca    1968
Glu Arg Asp Met Arg Ser Leu Leu Pro Met Pro Gly Ala Ala Ser Pro
            645             650             655

cac aaa cct gtt cta gta ggt gat ctg aaa atc gca gac ttc aag cag    2016
His Lys Pro Val Leu Val Gly Asp Leu Lys Ile Ala Asp Phe Lys Gln
            660             665             670

ttt ctg tcg agc aag ggt gtt cag gta gaa ttt gca ggt gga gga gct    2064
Phe Leu Ser Ser Lys Gly Val Gln Val Glu Phe Ala Gly Gly Gly Ala
            675             680             685

tta cgt tgt ggt gaa tat gtc act cta cga aag gtt gga ccg acg ggt    2112
Leu Arg Cys Gly Glu Tyr Val Thr Leu Arg Lys Val Gly Pro Thr Gly
    690             695             700

caa aag gga gga gca tcg ggt cca cag caa att ctg ata gaa gga ccg    2160
Gln Lys Gly Gly Ala Ser Gly Pro Gln Gln Ile Leu Ile Glu Gly Pro
705             710             715             720

ttg tgt gaa gac tat tac aaa atc agg gat tat ctc tat tct cag ttc    2208
Leu Cys Glu Asp Tyr Tyr Lys Ile Arg Asp Tyr Leu Tyr Ser Gln Phe
            725             730             735

tac ctc ctc tga                                                    2220
Tyr Leu Leu
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<210> 34

<211> 739

<212> PRT

<213> Arabidopsis thaliana

<400> 34

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Met Gly Thr Ser Val Gln Val Thr Pro Leu Cys Gly Val Tyr Asn Glu
1               5               10              15


Asn Pro Leu Ser Tyr Leu Val Ser Ile Asp Gly Phe Asn Phe Leu Ile
            20              25              30


Asp Cys Gly Trp Asn Asp Leu Phe Asp Thr Ser Leu Leu Glu Pro Leu
            35              40              45
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Pro Arg Val Ala Ser Thr Ile Asp Ala Val Leu Leu Ser His Pro Asp
    50   55   60

Thr Leu His Ile Gly Ala Leu Pro Tyr Ala Met Lys Gln Leu Gly Leu
65   70   75   80

Ser Ala Pro Val Tyr Ala Thr Glu Pro Val His Arg Leu Gly Leu Leu
                85   90   95

Thr Met Tyr Asp Gln Phe Leu Ser Arg Lys Gln Val Ser Asp Phe Asp
            100   105   110

Leu Phe Thr Leu Asp Asp Ile Asp Ser Ala Phe Gln Asn Val Ile Arg
        115   120   125

Leu Thr Tyr Ser Gln Asn Tyr His Leu Ser Gly Lys Gly Glu Gly Ile
        130   135   140

Val Ile Ala Pro His Val Ala Gly His Met Leu Gly Gly Ser Ile Trp
145   150   155   160

Arg Ile Thr Lys Asp Gly Glu Asp Val Ile Tyr Ala Val Asp Tyr Asn
                165   170   175

His Arg Lys Glu Arg His Leu Asn Gly Thr Val Leu Gln Ser Phe Val
            180   185   190

Arg Pro Ala Val Leu Ile Thr Asp Ala Tyr His Ala Leu Tyr Thr Asn
        195   200   205

Gln Thr Ala Arg Gln Gln Arg Asp Lys Glu Phe Leu Asp Thr Ile Ser
    210   215   220

Lys His Leu Glu Val Gly Gly Asn Val Leu Leu Pro Val Asp Thr Ala
225   230   235   240

Gly Arg Val Leu Glu Leu Leu Leu Ile Leu Glu Gln His Trp Ser Gln
                245   250   255

Arg Gly Phe Ser Phe Pro Ile Tyr Phe Leu Thr Tyr Val Ser Ser Ser
            260   265   270

Thr Ile Asp Tyr Val Lys Ser Phe Leu Glu Trp Met Ser Asp Ser Ile
        275   280   285

84

Ser Lys Ser Phe Glu Thr Ser Arg Asp Asn Ala Phe Leu Leu Arg His
    290   295   300

Val Thr Leu Leu Ile Asn Lys Thr Asp Leu Asp Asn Ala Pro Pro Gly
305   310   315   320

Pro Lys Val Val Leu Ala Ser Met Ala Ser Leu Glu Ala Gly Phe Ala
            325   330   335

Arg Glu Ile Phe Val Glu Trp Ala Asn Asp Pro Arg Asn Leu Val Leu
            340   345   350

Phe Thr Glu Thr Gly Gln Phe Gly Thr Leu Ala Arg Met Leu Gln Ser
        355   360   365

Ala Pro Pro Pro Lys Phe Val Lys Val Thr Met Ser Lys Arg Val Pro
    370   375   380

Leu Ala Gly Glu Glu Leu Ile Ala Tyr Glu Glu Glu Gln Asn Arg Leu
385   390   395   400

Lys Arg Glu Glu Ala Leu Arg Ala Ser Leu Val Lys Glu Glu Glu Thr
            405   410   415

Lys Ala Ser His Gly Ser Asp Asp Asn Ser Ser Glu Pro Met Ile Ile
            420   425   430

Asp Thr Lys Thr Thr His Asp Val Val Gly Ser His Gly Pro Ala Tyr
        435   440   445

Lys Asp Ile Leu Ile Asp Gly Phe Val Pro Pro Ser Ser Ser Val Ala
    450   455   460

Pro Met Phe Pro Tyr Tyr Asp Asn Thr Ser Glu Trp Asp Asp Phe Gly
465   470   475   480

Glu Ile Ile Asn Pro Asp Asp Tyr Val Ile Lys Asp Glu Asp Met Asp
            485   490   495

Arg Gly Ala Met His Asn Gly Gly Asp Val Asp Gly Arg Leu Asp Glu
            500   505   510

Ala Thr Ala Ser Leu Met Leu Asp Thr Arg Pro Ser Lys Val Met Ser
    515   520   525

85

Asn Glu Leu Ile Val Thr Val Ser Cys Ser Leu Val Lys Met Asp Tyr
530   535   540

Glu Gly Arg Ser Asp Gly Arg Ser Ile Lys Ser Met Ile Ala His Val
545   550   555   560

Ser Pro Leu Lys Leu Val Leu Val His Ala Ile Ala Glu Ala Thr Glu
                565   570   575

His Leu Lys Gln His Cys Leu Asn Asn Ile Cys Pro His Val Tyr Ala
                580   585   590

Pro Gln Ile Glu Glu Thr Val Asp Val Thr Ser Asp Leu Cys Ala Tyr
            595   600   605

Lys Val Gln Leu Ser Glu Lys Leu Met Ser Asn Val Ile Phe Lys Lys
        610   615   620

Leu Gly Asp Ser Glu Val Ala Trp Val Asp Ser Glu Val Gly Lys Thr
625   630   635   640

Glu Arg Asp Met Arg Ser Leu Leu Pro Met Pro Gly Ala Ala Ser Pro
                645   650   655

His Lys Pro Val Leu Val Gly Asp Leu Lys Ile Ala Asp Phe Lys Gln
                660   665   670

Phe Leu Ser Ser Lys Gly Val Gln Val Glu Phe Ala Gly Gly Gly Ala
        675   680   685

Leu Arg Cys Gly Glu Tyr Val Thr Leu Arg Lys Val Gly Pro Thr Gly
        690   695   700

Gln Lys Gly Gly Ala Ser Gly Pro Gln Gln Ile Leu Ile Glu Gly Pro
705   710   715   720

Leu Cys Glu Asp Tyr Tyr Lys Ile Arg Asp Tyr Leu Tyr Ser Gln Phe
                725   730   735

Tyr Leu Leu

<210> 35

<211> 1116

<212>   DNA

<213>   Arabidopsis thaliana

<220>

<221>   CDS

<222>   (1)..(1116)

<223>

<400>   35

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Met Ala Ala Ala Met Ser Ser Ser Cys Cys Ala Ser Ser Leu Arg Leu
1               5                   10                  15

atc cca ttc aaa cgg acc ttg ttt tct tca atc cat tat ccg gcc aaa        96
Ile Pro Phe Lys Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys
                20                  25                  30

acc ctt ctt cta cga cca cta aaa ccg tcg gaa gtt cct tcc ttt cgc       144
Thr Leu Leu Leu Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg
            35                  40                  45

cgg acg atc atc act ttc cag aaa att tca acc ggg att gtt cct cca       192
Arg Thr Ile Ile Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro
        50                  55                  60

cca tcg gct tca tca tct ccg tcg agc tat gga gac ctt caa cca atc       240
Pro Ser Ala Ser Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile
65                  70                  75                  80

gaa gag ctt cca ccg aag cta caa gag atc gtc aag ctt ttc caa tcg       288
Glu Glu Leu Pro Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser
                85                  90                  95

gta caa gag cca aag gct aaa tac gag cag ctt atg ttc tac ggg aag       336
Val Gln Glu Pro Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys
                100                 105                 110

aat ctg aca cct ctc gat tct caa ttc aag acg agg gag aat aaa gta       384
Asn Leu Thr Pro Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val
            115                 120                 125

gaa gga tgt gtt tct cag gtt tgg gtt agg gct ttc ttt gat gag gaa       432
Glu Gly Cys Val Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu
        130                 135                 140

cgt aat gtt gtg tat gaa gct gat tct gat tcg gtt ctc act aaa ggg       480
Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly
145                 150                 155                 160

tta gct gct cta tta gtc aag ggt tta tct gga aga cct gtc cct gag       528
Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu
                165                 170                 175
```

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att ttg agg ata aca cct gat ttc gct gtt ctt ctc ggg ttg cag cag    576
Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln
            180                 185                 190

agt ctg tct cct tct aga aac aat gga tta ctt aat atg ctt aag ctg    624
Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu
            195                 200                 205

atg cag aaa aag gct ctt cat ttg gaa gtc aaa ggt gag gaa gat tca    672
Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser
        210                 215                 220

agt tct gga gag agt tca gaa tcc agc ttt gtg tct att cct gag act    720
Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr
225                 230                 235                 240

aag gac gaa gct aat gtt ccg gag gtg gat ttg gag tct aaa cct gat    768
Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp
                245                 250                 255

cta gtt gag gat ttg gga aca gaa aag att gat gat tct gag agt ggg    816
Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly
            260                 265                 270

tca aat gtt gtt gct tta ggg agt aga ggg atg agg ata aga gag aaa    864
Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys
            275                 280                 285

ttg gag aag gag cta gat cct gtt gag tta gaa gtt gaa gat gtt tct    912
Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser
        290                 295                 300

tac cag cac gca gga cat gcc gct gtt aga ggt agt gct ggt gat gat    960
Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp
305                 310                 315                 320

ggg gaa aca cat ttc aac ttg cga atc gtt tcg gat gct ttc caa ggt   1008
Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly
                325                 330                 335

aaa agc ttg gtc aag aga cat agg ctg ata tat gac ttg ttg caa gat   1056
Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp
            340                 345                 350

gag ttg aag agc ggg tta cat gct ctc tct att gtg gca aag act cct   1104
Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro
            355                 360                 365

gct gag gtt tga                                                    1116
Ala Glu Val
        370
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<210>    36

<211>    371

<212>    PRT
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<213> Arabidopsis thaliana

<400> 36

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1   5   10   15

Ile Pro Phe Lys Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys
            20   25   30

Thr Leu Leu Leu Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg
        35   40   45

Arg Thr Ile Ile Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro
    50   55   60

Pro Ser Ala Ser Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile
65   70   75   80

Glu Glu Leu Pro Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser
                85   90   95

Val Gln Glu Pro Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys
            100   105   110

Asn Leu Thr Pro Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val
        115   120   125

Glu Gly Cys Val Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu
    130   135   140

Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly
145   150   155   160

Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu
                165   170   175

Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln
            180   185   190

Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu
        195   200   205

Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser
    210   215   220

89

```
Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr
225             230             235             240

Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp
            245             250             255

Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly
            260             265             270

Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys
            275             280             285

Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser
    290             295             300

Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp
305             310             315             320

Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly
            325             330             335

Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp
            340             345             350

Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro
    355             360             365

Ala Glu Val
    370
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<210> 37

<211> 1059

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1059)

<223> 20933

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Met Asp Leu Met Glu Lys Asn Leu Glu Leu Val Glu Ile Gln Lys Leu
1               5                   10                  15

gaa ggc cac acc gat cgt gtt tgg agc gta gct tgg aac ccc gtt tct        96
Glu Gly His Thr Asp Arg Val Trp Ser Val Ala Trp Asn Pro Val Ser
            20                  25                  30

tct cac gcc gac ggt gtt tca ccg att ctt gct tct tgc agt ggc gat       144
Ser His Ala Asp Gly Val Ser Pro Ile Leu Ala Ser Cys Ser Gly Asp
        35                  40                  45

aac act gtt cga atc tgg gaa caa agc tct ctc tct cgc tcc tgg act       192
Asn Thr Val Arg Ile Trp Glu Gln Ser Ser Leu Ser Arg Ser Trp Thr
        50                  55                  60

tgc aag aca gtt ttg gaa gag acg cat aca aga act gtg agg tcg tgc       240
Cys Lys Thr Val Leu Glu Glu Thr His Thr Arg Thr Val Arg Ser Cys
65                  70                  75                  80

gct tgg tca ccc tca gga cag tta ttg gcc act gca agt ttt gat ggt       288
Ala Trp Ser Pro Ser Gly Gln Leu Leu Ala Thr Ala Ser Phe Asp Gly
                85                  90                  95

acc act ggc att tgg aag aat tac ggt tct gag ttt gag tgt att tcc       336
Thr Thr Gly Ile Trp Lys Asn Tyr Gly Ser Glu Phe Glu Cys Ile Ser
            100                 105                 110

act ttg gag gga cat gaa aac gaa gtc aaa agt gta tca tgg aat gca       384
Thr Leu Glu Gly His Glu Asn Glu Val Lys Ser Val Ser Trp Asn Ala
            115                 120                 125

tct ggt tca tgc ctt gca aca tgt agt aga gat aag tct gtt tgg att       432
Ser Gly Ser Cys Leu Ala Thr Cys Ser Arg Asp Lys Ser Val Trp Ile
        130                 135                 140

tgg gaa gtg ctt gaa ggg aat gaa tat gac tgt gct gcg gta tta act       480
Trp Glu Val Leu Glu Gly Asn Glu Tyr Asp Cys Ala Ala Val Leu Thr
145                 150                 155                 160

ggg cat aca caa gat gtg aag atg gtt cag tgg cat ccc acc atg gat       528
Gly His Thr Gln Asp Val Lys Met Val Gln Trp His Pro Thr Met Asp
                165                 170                 175

gtt tta ttt tct tgc agt tat gat aac acc atc aag gtt tgg tgg tct       576
Val Leu Phe Ser Cys Ser Tyr Asp Asn Thr Ile Lys Val Trp Trp Ser
            180                 185                 190

gaa gat gat gat ggt gag tat caa tgt gtc caa acc tta ggt gaa tct       624
Glu Asp Asp Asp Gly Glu Tyr Gln Cys Val Gln Thr Leu Gly Glu Ser
            195                 200                 205

aac aac ggt cac tct tca acg gta tgg tcc atc tca ttt aac gct gca       672
Asn Asn Gly His Ser Ser Thr Val Trp Ser Ile Ser Phe Asn Ala Ala
        210                 215                 220

ggg gac aag atg gtc act tgt agt gat gat cta acc ttg aag ata tgg       720
```

91

```
Gly Asp Lys Met Val Thr Cys Ser Asp Asp Leu Thr Leu Lys Ile Trp
225             230             235             240

ggg aca gat att gcc aag atg cag tct ggt gaa gaa tat gca cct tgg    768
Gly Thr Asp Ile Ala Lys Met Gln Ser Gly Glu Glu Tyr Ala Pro Trp
                245             250             255

att cat ctt tgt act ctc tct ggc tat cat gac cgt acc ata tac tca    816
Ile His Leu Cys Thr Leu Ser Gly Tyr His Asp Arg Thr Ile Tyr Ser
                260             265             270

gct cac tgg tca agg gac gac att att gcc agt gga gca ggc gat aat    864
Ala His Trp Ser Arg Asp Asp Ile Ile Ala Ser Gly Ala Gly Asp Asn
            275             280             285

gct ata cgg ttg ttt gtg gac agc aaa cat gac tct gtt gat gga cct    912
Ala Ile Arg Leu Phe Val Asp Ser Lys His Asp Ser Val Asp Gly Pro
        290             295             300

tca tat aat ctt ttg ctg aag aag aat aaa gca cat gaa aat gat gta    960
Ser Tyr Asn Leu Leu Leu Lys Lys Asn Lys Ala His Glu Asn Asp Val
305             310             315             320

aac tct gtc caa tgg tca ccc ggt gag ggg aac cgg ttg ctt gcg tcg   1008
Asn Ser Val Gln Trp Ser Pro Gly Glu Gly Asn Arg Leu Leu Ala Ser
                325             330             335

gct agt gat gat ggg atg gtc aag att tgg cag ctt gca act aaa ccg   1056
Ala Ser Asp Asp Gly Met Val Lys Ile Trp Gln Leu Ala Thr Lys Pro
            340             345             350

tga                                                                1059
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<210> 38

<211> 352

<212> PRT

<213> Arabidopsis thaliana

<400> 38

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Met Asp Leu Met Glu Lys Asn Leu Glu Leu Val Glu Ile Gln Lys Leu
1               5               10              15

Glu Gly His Thr Asp Arg Val Trp Ser Val Ala Trp Asn Pro Val Ser
            20              25              30

Ser His Ala Asp Gly Val Ser Pro Ile Leu Ala Ser Cys Ser Gly Asp
            35              40              45

Asn Thr Val Arg Ile Trp Glu Gln Ser Ser Leu Ser Arg Ser Trp Thr
50              55              60
```

92

Cys Lys Thr Val Leu Glu Glu Thr His Thr Arg Thr Val Arg Ser Cys
65   70   75   80

Ala Trp Ser Pro Ser Gly Gln Leu Leu Ala Thr Ala Ser Phe Asp Gly
            85   90   95

Thr Thr Gly Ile Trp Lys Asn Tyr Gly Ser Glu Phe Glu Cys Ile Ser
            100   105   110

Thr Leu Glu Gly His Glu Asn Glu Val Lys Ser Val Ser Trp Asn Ala
        115   120   125

Ser Gly Ser Cys Leu Ala Thr Cys Ser Arg Asp Lys Ser Val Trp Ile
    130   135   140

Trp Glu Val Leu Glu Gly Asn Glu Tyr Asp Cys Ala Ala Val Leu Thr
145   150   155   160

Gly His Thr Gln Asp Val Lys Met Val Gln Trp His Pro Thr Met Asp
            165   170   175

Val Leu Phe Ser Cys Ser Tyr Asp Asn Thr Ile Lys Val Trp Trp Ser
            180   185   190

Glu Asp Asp Asp Gly Glu Tyr Gln Cys Val Gln Thr Leu Gly Glu Ser
    195   200   205

Asn Asn Gly His Ser Ser Thr Val Trp Ser Ile Ser Phe Asn Ala Ala
    210   215   220

Gly Asp Lys Met Val Thr Cys Ser Asp Asp Leu Thr Leu Lys Ile Trp
225   230   235   240

Gly Thr Asp Ile Ala Lys Met Gln Ser Gly Glu Glu Tyr Ala Pro Trp
            245   250   255

Ile His Leu Cys Thr Leu Ser Gly Tyr His Asp Arg Thr Ile Tyr Ser
            260   265   270

Ala His Trp Ser Arg Asp Asp Ile Ile Ala Ser Gly Ala Gly Asp Asn
    275   280   285

Ala Ile Arg Leu Phe Val Asp Ser Lys His Asp Ser Val Asp Gly Pro
    290   295   300

93

Ser Tyr Asn Leu Leu Leu Lys Lys Asn Lys Ala His Glu Asn Asp Val
305   310   315   320

Asn Ser Val Gln Trp Ser Pro Gly Glu Gly Asn Arg Leu Leu Ala Ser
                325   330   335

Ala Ser Asp Asp Gly Met Val Lys Ile Trp Gln Leu Ala Thr Lys Pro
            340   345   350

<210> 39

<211> 942

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(924)

<223>

<400> 39
atg cta agc ttg aga tat tca tta cct tat ctt ctt ctt caa aca agg   48
Met Leu Ser Leu Arg Tyr Ser Leu Pro Tyr Leu Leu Leu Gln Thr Arg
1   5   10   15

gaa tca tca act aag ctc ttc acc aaa aag cct aac aat gtt gtg gtt   96
Glu Ser Ser Thr Lys Leu Phe Thr Lys Lys Pro Asn Asn Val Val Val
                20   25   30

tgt gcg gcg aga ggt cca aga cct cgg tct cct cgt gta tgg aaa aca   144
Cys Ala Ala Arg Gly Pro Arg Pro Arg Ser Pro Arg Val Trp Lys Thr
            35   40   45

agg aag agg att gga act atc tct aaa gct gcc aaa atg att gct tgt   192
Arg Lys Arg Ile Gly Thr Ile Ser Lys Ala Ala Lys Met Ile Ala Cys
        50   55   60

ata aaa gga ttg tcg aat gtt aaa gaa gaa gtt tat gga gcg ctt gat   240
Ile Lys Gly Leu Ser Asn Val Lys Glu Glu Val Tyr Gly Ala Leu Asp
65   70   75   80

tcc ttc att gct tgg gaa tta gag ttc cct ctt gtt ata gtt aag aag   288
Ser Phe Ile Ala Trp Glu Leu Glu Phe Pro Leu Val Ile Val Lys Lys
                85   90   95

gca tta gtt ata ctt gaa gat gaa aaa gaa tgg aag aag att att cag   336
Ala Leu Val Ile Leu Glu Asp Glu Lys Glu Trp Lys Lys Ile Ile Gln

94

```
                100                    105                    110
gtg aca aaa tgg atg ctg agt aaa ggc caa gga aga aca atg gga act    384
Val Thr Lys Trp Met Leu Ser Lys Gly Gln Gly Arg Thr Met Gly Thr
        115                    120                    125

tac ttc tca tta cta aat gct tta gca gaa gat aat cgc ctt gac gaa    432
Tyr Phe Ser Leu Leu Asn Ala Leu Ala Glu Asp Asn Arg Leu Asp Glu
    130                    135                    140

gct gag gaa ttg tgg aac aaa ttg ttc atg gaa cat tta gaa gga act    480
Ala Glu Glu Leu Trp Asn Lys Leu Phe Met Glu His Leu Glu Gly Thr
145                    150                    155                    160

cct aga aag ttc ttc aac aaa atg atc tct ata tat tac aag aga gat    528
Pro Arg Lys Phe Phe Asn Lys Met Ile Ser Ile Tyr Tyr Lys Arg Asp
                    165                    170                    175

atg cac caa aag ctc ttc gag gtc ttt gct gac atg gag gag ctt gga    576
Met His Gln Lys Leu Phe Glu Val Phe Ala Asp Met Glu Glu Leu Gly
                180                    185                    190

gtg aaa ccg aat gtt gcg att gtg tct atg gtt gga aaa gtg ttt gtg    624
Val Lys Pro Asn Val Ala Ile Val Ser Met Val Gly Lys Val Phe Val
            195                    200                    205

aaa cta gag atg aag gat aag tac gag aaa ctg atg aag aaa tat cct    672
Lys Leu Glu Met Lys Asp Lys Tyr Glu Lys Leu Met Lys Lys Tyr Pro
        210                    215                    220

cca cca cag tgg gag ttt aga tac atc aaa gga aga cgt gtt aag gtc    720
Pro Pro Gln Trp Glu Phe Arg Tyr Ile Lys Gly Arg Arg Val Lys Val
225                    230                    235                    240

aag gca aag cag ctg aat gag cta agc gaa ggt gaa ggt ggt tta agc    768
Lys Ala Lys Gln Leu Asn Glu Leu Ser Glu Gly Glu Gly Gly Leu Ser
                    245                    250                    255

agc gac gaa gat aag att gac aat gag att gag agt gaa gaa gaa gat    816
Ser Asp Glu Asp Lys Ile Asp Asn Glu Ile Glu Ser Glu Glu Glu Asp
                260                    265                    270

ggt gag gat ctc agt gaa gag gaa gaa gat gaa aaa gaa ctt ttg ggt    864
Gly Glu Asp Leu Ser Glu Glu Glu Glu Asp Glu Lys Glu Leu Leu Gly
            275                    280                    285

gga agt caa gga cag att act tct aga gaa ccc agt ctt gat cat ttg    912
Gly Ser Gln Gly Gln Ile Thr Ser Arg Glu Pro Ser Leu Asp His Leu
        290                    295                    300

gac tct tca tga                                                    924
Asp Ser Ser
305
```

```
<210>   40

<211>   307
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<212> PRT

<213> Arabidopsis thaliana

<400> 40

Met Leu Ser Leu Arg Tyr Ser Leu Pro Tyr Leu Leu Leu Gln Thr Arg
1   5   10   15

Glu Ser Ser Thr Lys Leu Phe Thr Lys Lys Pro Asn Asn Val Val Val
            20   25   30

Cys Ala Ala Arg Gly Pro Arg Pro Arg Ser Pro Arg Val Trp Lys Thr
        35   40   45

Arg Lys Arg Ile Gly Thr Ile Ser Lys Ala Ala Lys Met Ile Ala Cys
    50   55   60

Ile Lys Gly Leu Ser Asn Val Lys Glu Glu Val Tyr Gly Ala Leu Asp
65   70   .   75   80

Ser Phe Ile Ala Trp Glu Leu Glu Phe Pro Leu Val Ile Val Lys Lys
                85   90   95

Ala Leu Val Ile Leu Glu Asp Glu Lys Glu Trp Lys Lys Ile Ile Gln
                100   105   110

Val Thr Lys Trp Met Leu Ser Lys Gly Gln Gly Arg Thr Met Gly Thr
            115   120   125

Tyr Phe Ser Leu Leu Asn Ala Leu Ala Glu Asp Asn Arg Leu Asp Glu
        130   135   140

Ala Glu Glu Leu Trp Asn Lys Leu Phe Met Glu His Leu Glu Gly Thr
145   150   155   160

Pro Arg Lys Phe Phe Asn Lys Met Ile Ser Ile Tyr Tyr Lys Arg Asp
                165   170   175

Met His Gln Lys Leu Phe Glu Val Phe Ala Asp Met Glu Glu Leu Gly
            180   185   190

Val Lys Pro Asn Val Ala Ile Val Ser Met Val Gly Lys Val Phe Val
        195   200   205

```
Lys Leu Glu Met Lys Asp Lys Tyr Glu Lys Leu Met Lys Lys Tyr Pro
    210             215             220
```

```
Pro Pro Gln Trp Glu Phe Arg Tyr Ile Lys Gly Arg Arg Val Lys Val
225             230             235             240
```

```
Lys Ala Lys Gln Leu Asn Glu Leu Ser Glu Gly Glu Gly Gly Leu Ser
            245             250             255
```

```
Ser Asp Glu Asp Lys Ile Asp Asn Glu Ile Glu Ser Glu Glu Glu Asp
            260             265             270
```

```
Gly Glu Asp Leu Ser Glu Glu Glu Glu Asp Glu Lys Glu Leu Leu Gly
            275             280             285
```

```
Gly Ser Gln Gly Gln Ile Thr Ser Arg Glu Pro Ser Leu Asp His Leu
    290             295             300
```

```
Asp Ser Ser
305
```

<210> 41

<211> 2427

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2427)

<223> 21878

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<400> 41
atg gta aag gaa act cta att cct ccg tca tct acg tca atg acg acc    48
Met Val Lys Glu Thr Leu Ile Pro Pro Ser Ser Thr Ser Met Thr Thr
1               5               10              15

gga aca tct tct tct tcg tct ctt tca atg acg tta tcc tca aca aac    96
Gly Thr Ser Ser Ser Ser Ser Leu Ser Met Thr Leu Ser Ser Thr Asn
            20              25              30

gcg tta tcg ttt ttg tcg aaa gga tgg aga gag gta tgg gat tca gca   144
Ala Leu Ser Phe Leu Ser Lys Gly Trp Arg Glu Val Trp Asp Ser Ala
```

```
              35                    40                    45

gat gcg gat ttg cag ctg atg cga gac aga gct aac tct gtt aag aat        192
Asp Ala Asp Leu Gln Leu Met Arg Asp Arg Ala Asn Ser Val Lys Asn
    50                    55                    60

cta gca tca acg ttc gat aga gag atc gag aat ttc ctc aat aac tcg        240
Leu Ala Ser Thr Phe Asp Arg Glu Ile Glu Asn Phe Leu Asn Asn Ser
65                    70                    75                    80

gcg agg tct gcg ttt ccc gtt ggt tca cca tcg gcg tcg tct ttc tca        288
Ala Arg Ser Ala Phe Pro Val Gly Ser Pro Ser Ala Ser Ser Phe Ser
                  85                    90                    95

aat gaa att ggt atc atg aag aag ctt cag ccg aag att tcg gag ttt        336
Asn Glu Ile Gly Ile Met Lys Lys Leu Gln Pro Lys Ile Ser Glu Phe
                  100                   105                   110

cgt agg gtt tat tcg gcg ccg gag att agt cgc aag gtt atg gag aga        384
Arg Arg Val Tyr Ser Ala Pro Glu Ile Ser Arg Lys Val Met Glu Arg
              115                   120                   125

tgg gga cct gcg aga gcg aag ctt gga atg gat cta tcg gcg att aag        432
Trp Gly Pro Ala Arg Ala Lys Leu Gly Met Asp Leu Ser Ala Ile Lys
    130                   135                   140

aag gcg att gtg tct gag atg gaa ttg gat gag cgt cag gga gtt ttg        480
Lys Ala Ile Val Ser Glu Met Glu Leu Asp Glu Arg Gln Gly Val Leu
145                   150                   155                   160

gag atg agt aga ttg agg aga cgg cgt aat agt gat agg gtt agg ttt        528
Glu Met Ser Arg Leu Arg Arg Arg Arg Asn Ser Asp Arg Val Arg Phe
                  165                   170                   175

acg gag ttt ttc gcg gag gct gag aga gat gga gaa gct tat ttc ggt        576
Thr Glu Phe Phe Ala Glu Ala Glu Arg Asp Gly Glu Ala Tyr Phe Gly
                  180                   185                   190

gat tgg gaa ccg att agg tct ttg aag agt aga ttt aaa gag ttt gag        624
Asp Trp Glu Pro Ile Arg Ser Leu Lys Ser Arg Phe Lys Glu Phe Glu
                  195                   200                   205

aaa cga agc tcg tta gaa ata ttg agt gga ttc aag aac agt gaa ttt        672
Lys Arg Ser Ser Leu Glu Ile Leu Ser Gly Phe Lys Asn Ser Glu Phe
    210                   215                   220

gtt gag aag ctc aaa acc agc ttt aaa tca att tac aaa gaa act gat        720
Val Glu Lys Leu Lys Thr Ser Phe Lys Ser Ile Tyr Lys Glu Thr Asp
225                   230                   235                   240

gag gct aag gat gtc cct ccg ttg gat gta cct gaa ctg ttg gca tgt        768
Glu Ala Lys Asp Val Pro Pro Leu Asp Val Pro Glu Leu Leu Ala Cys
                  245                   250                   255

ttg gtt aga caa tct gaa cct ttt ctt gat cag att ggt gtt aga aag        816
Leu Val Arg Gln Ser Glu Pro Phe Leu Asp Gln Ile Gly Val Arg Lys
                  260                   265                   270

gat aca tgt gac cga ata gta gaa agc ctt tgc aaa tgc aag agc caa        864
Asp Thr Cys Asp Arg Ile Val Glu Ser Leu Cys Lys Cys Lys Ser Gln
```

98

```
                 275                  280                   285

caa ctt tgg cgt ctg cca tct gca caa gca tcc gat tta att gaa aat      912
Gln Leu Trp Arg Leu Pro Ser Ala Gln Ala Ser Asp Leu Ile Glu Asn
        290                  295                   300

gat aac cat gga gtt gat ttg gat atg agg ata gcc agt gtt ctt caa      960
Asp Asn His Gly Val Asp Leu Asp Met Arg Ile Ala Ser Val Leu Gln
305                  310                   315                   320

agc aca gga cac cat tat gat ggt ggg ttt tgg act gat ttt gtg aag     1008
Ser Thr Gly His His Tyr Asp Gly Gly Phe Trp Thr Asp Phe Val Lys
                     325                  330                   335

cct gag aca ccg gaa aac aaa agg cat gtg gca att gtt aca aca gct     1056
Pro Glu Thr Pro Glu Asn Lys Arg His Val Ala Ile Val Thr Thr Ala
            340                  345                   350

agt ctt cct tgg atg acc gga aca gct gta aat ccg cta ttc aga gcg     1104
Ser Leu Pro Trp Met Thr Gly Thr Ala Val Asn Pro Leu Phe Arg Ala
            355                  360                   365

gcg tat ttg gca aaa gct gca aaa cag agt gtt act ctc gtg gtt cct     1152
Ala Tyr Leu Ala Lys Ala Ala Lys Gln Ser Val Thr Leu Val Val Pro
        370                  375                   380

tgg ctc tgc gaa tct gat caa gaa cta gtg tat cca aac aat ctc acc     1200
Trp Leu Cys Glu Ser Asp Gln Glu Leu Val Tyr Pro Asn Asn Leu Thr
385                  390                   395                   400

ttc agc tca cct gaa gaa caa gag agt tat ata cgt aaa tgg ttg gag     1248
Phe Ser Ser Pro Glu Glu Gln Glu Ser Tyr Ile Arg Lys Trp Leu Glu
                405                  410                   415

gaa agg att ggt ttc aag gct gat ttt aaa atc tcc ttt tac cca gga     1296
Glu Arg Ile Gly Phe Lys Ala Asp Phe Lys Ile Ser Phe Tyr Pro Gly
            420                  425                   430

aag ttt tca aaa gaa agg cgc agc ata ttt cct gct ggt gac act tct     1344
Lys Phe Ser Lys Glu Arg Arg Ser Ile Phe Pro Ala Gly Asp Thr Ser
        435                  440                   445

caa ttt ata tcg tca aaa gat gct gac att gct ata ctt gaa gaa cct     1392
Gln Phe Ile Ser Ser Lys Asp Ala Asp Ile Ala Ile Leu Glu Glu Pro
        450                  455                   460

gaa cat ctc aac tgg tat tat cac ggc aag cgt tgg act gat aaa ttc     1440
Glu His Leu Asn Trp Tyr Tyr His Gly Lys Arg Trp Thr Asp Lys Phe
465                  470                   475                   480

aac cat gtt gtt gga att gtc cac aca aac tac tta gag tac atc aag     1488
Asn His Val Val Gly Ile Val His Thr Asn Tyr Leu Glu Tyr Ile Lys
                     485                  490                   495

agg gag aag aat gga gct ctt caa gca ttt ttt gtg aac cat gta aac     1536
Arg Glu Lys Asn Gly Ala Leu Gln Ala Phe Phe Val Asn His Val Asn
                500                  505                   510

aat tgg gtc aca cga gcg tat tgt gac aag gtt ctt cgc ctc tct gcg     1584
Asn Trp Val Thr Arg Ala Tyr Cys Asp Lys Val Leu Arg Leu Ser Ala
```

99

```
                    515                      520                      525
    gca aca caa gat tta cca aag tct gtt gta tgc aat gtc cat ggt gtc    1632
    Ala Thr Gln Asp Leu Pro Lys Ser Val Val Cys Asn Val His Gly Val
        530                     535                     540

    aat ccc aag ttc ctt atg att ggg gag aaa att gct gaa gag aga tcc    1680
    Asn Pro Lys Phe Leu Met Ile Gly Glu Lys Ile Ala Glu Glu Arg Ser
    545                     550                     555                     560

    cgt ggt gaa caa gct ttc tca aaa ggt gca tac ttc tta gga aaa atg    1728
    Arg Gly Glu Gln Ala Phe Ser Lys Gly Ala Tyr Phe Leu Gly Lys Met
                        565                     570                     575

    gtg tgg gct aaa gga tac aga gaa cta ata gat ctg atg gct aaa cac    1776
    Val Trp Ala Lys Gly Tyr Arg Glu Leu Ile Asp Leu Met Ala Lys His
                    580                     585                     590

    aaa agc gaa ctt ggg agc ttc aat cta gat gta tat ggg aac ggt gaa    1824
    Lys Ser Glu Leu Gly Ser Phe Asn Leu Asp Val Tyr Gly Asn Gly Glu
                595                     600                     605

    gat gca gtc gag gtc caa cgt gca gca aag aaa cat gac ttg aat ctc    1872
    Asp Ala Val Glu Val Gln Arg Ala Ala Lys Lys His Asp Leu Asn Leu
        610                     615                     620

    aat ttc ctc aaa gga agg gac cac gct gac gat gct ctt cac aag tac    1920
    Asn Phe Leu Lys Gly Arg Asp His Ala Asp Asp Ala Leu His Lys Tyr
    625                     630                     635                     640

    aaa gtg ttc ata aac ccc agc atc agc gat gtt cta tgc aca gca acc    1968
    Lys Val Phe Ile Asn Pro Ser Ile Ser Asp Val Leu Cys Thr Ala Thr
                        645                     650                     655

    gca gaa gca cta gcc atg ggg aag ttt gtg gtg tgt gca gat cac cct    2016
    Ala Glu Ala Leu Ala Met Gly Lys Phe Val Val Cys Ala Asp His Pro
                660                     665                     670

    tca aac gaa ttc ttt aga tca ttc ccg aac tgc tta act tac aaa aca    2064
    Ser Asn Glu Phe Phe Arg Ser Phe Pro Asn Cys Leu Thr Tyr Lys Thr
                675                     680                     685

    tcc gaa gac ttt gtg tcc aaa gtg caa gaa gca atg acg aaa gag cca    2112
    Ser Glu Asp Phe Val Ser Lys Val Gln Glu Ala Met Thr Lys Glu Pro
        690                     695                     700

    cta cct ctc act cct gaa caa atg tac aat ctc tct tgg gaa gca gca    2160
    Leu Pro Leu Thr Pro Glu Gln Met Tyr Asn Leu Ser Trp Glu Ala Ala
    705                     710                     715                     720

    aca cag agg ttc atg gag tat tca gat ctc gat aag atc tta aac aat    2208
    Thr Gln Arg Phe Met Glu Tyr Ser Asp Leu Asp Lys Ile Leu Asn Asn
                        725                     730                     735

    gga gag gga gga agg aag atg cga aaa tca aga tcg gtt ccg agc ttt    2256
    Gly Glu Gly Gly Arg Lys Met Arg Lys Ser Arg Ser Val Pro Ser Phe
                740                     745                     750

    aac gag gtg gtc gat gga gga ttg gca ttc tca cac tat gtt cta aca    2304
    Asn Glu Val Val Asp Gly Gly Leu Ala Phe Ser His Tyr Val Leu Thr
```

```
                755                   760                    765

ggg aac gat ttc ttg aga cta tgc act gga gca aca cca aga aca aaa    2352
Gly Asn Asp Phe Leu Arg Leu Cys Thr Gly Ala Thr Pro Arg Thr Lys
        770                 775                 780

gac tat gat aat caa cat tgc aag gat ctg aat ctc gta cca cct cac    2400
Asp Tyr Asp Asn Gln His Cys Lys Asp Leu Asn Leu Val Pro Pro His
785                 790                 795                 800

gtt cac aag cca atc ttc ggc tgg tag                                2427
Val His Lys Pro Ile Phe Gly Trp
                805
```

<210> 42

<211> 808

<212> PRT

<213> Arabidopsis thaliana

<400> 42

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Met Val Lys Glu Thr Leu Ile Pro Pro Ser Ser Thr Ser Met Thr Thr
1               5               10                  15


Gly Thr Ser Ser Ser Ser Ser Leu Ser Met Thr Leu Ser Ser Thr Asn
            20              25                  30


Ala Leu Ser Phe Leu Ser Lys Gly Trp Arg Glu Val Trp Asp Ser Ala
        35              40                  45


Asp Ala Asp Leu Gln Leu Met Arg Asp Arg Ala Asn Ser Val Lys Asn
    50              55                  60


Leu Ala Ser Thr Phe Asp Arg Glu Ile Glu Asn Phe Leu Asn Asn Ser
65              70                  75                  80


Ala Arg Ser Ala Phe Pro Val Gly Ser Pro Ser Ala Ser Ser Phe Ser
                85              90                  95


Asn Glu Ile Gly Ile Met Lys Lys Leu Gln Pro Lys Ile Ser Glu Phe
            100             105                 110


Arg Arg Val Tyr Ser Ala Pro Glu Ile Ser Arg Lys Val Met Glu Arg
        115             120                 125


Trp Gly Pro Ala Arg Ala Lys Leu Gly Met Asp Leu Ser Ala Ile Lys
```

101

```
          130                    135                     140

Lys Ala Ile Val Ser Glu Met Glu Leu Asp Glu Arg Gln Gly Val Leu
145                     150                 155                 160

Glu Met Ser Arg Leu Arg Arg Arg Arg Asn Ser Asp Arg Val Arg Phe
                    165                 170                 175

Thr Glu Phe Phe Ala Glu Ala Glu Arg Asp Gly Glu Ala Tyr Phe Gly
            180                 185                 190

Asp Trp Glu Pro Ile Arg Ser Leu Lys Ser Arg Phe Lys Glu Phe Glu
            195                 200                 205

Lys Arg Ser Ser Leu Glu Ile Leu Ser Gly Phe Lys Asn Ser Glu Phe
        210                 215                 220

Val Glu Lys Leu Lys Thr Ser Phe Lys Ser Ile Tyr Lys Glu Thr Asp
225                 230                 235                 240

Glu Ala Lys Asp Val Pro Pro Leu Asp Val Pro Glu Leu Leu Ala Cys
                245                 250                 255

Leu Val Arg Gln Ser Glu Pro Phe Leu Asp Gln Ile Gly Val Arg Lys
            260                 265                 270

Asp Thr Cys Asp Arg Ile Val Glu Ser Leu Cys Lys Cys Lys Ser Gln
        275                 280                 285

Gln Leu Trp Arg Leu Pro Ser Ala Gln Ala Ser Asp Leu Ile Glu Asn
        290                 295                 300

Asp Asn His Gly Val Asp Leu Asp Met Arg Ile Ala Ser Val Leu Gln
305                 310                 315                 320

Ser Thr Gly His His Tyr Asp Gly Gly Phe Trp Thr Asp Phe Val Lys
            325                 330                 335

Pro Glu Thr Pro Glu Asn Lys Arg His Val Ala Ile Val Thr Thr Ala
            340                 345                 350

Ser Leu Pro Trp Met Thr Gly Thr Ala Val Asn Pro Leu Phe Arg Ala
            355                 360                 365

Ala Tyr Leu Ala Lys Ala Ala Lys Gln Ser Val Thr Leu Val Val Pro
```

102

                370   375   380

Trp Leu Cys Glu Ser Asp Gln Glu Leu Val Tyr Pro Asn Asn Leu Thr
385   390   395   400

Phe Ser Ser Pro Glu Glu Gln Glu Ser Tyr Ile Arg Lys Trp Leu Glu
                405   410   415

Glu Arg Ile Gly Phe Lys Ala Asp Phe Lys Ile Ser Phe Tyr Pro Gly
                420   425   430

Lys Phe Ser Lys Glu Arg Arg Ser Ile Phe Pro Ala Gly Asp Thr Ser
                435   440   445

Gln Phe Ile Ser Ser Lys Asp Ala Asp Ile Ala Ile Leu Glu Glu Pro
                450   455   460

Glu His Leu Asn Trp Tyr Tyr His Gly Lys Arg Trp Thr Asp Lys Phe
465   470   475   480

Asn His Val Val Gly Ile Val His Thr Asn Tyr Leu Glu Tyr Ile Lys
                485   490   495

Arg Glu Lys Asn Gly Ala Leu Gln Ala Phe Phe Val Asn His Val Asn
                500   505   510

Asn Trp Val Thr Arg Ala Tyr Cys Asp Lys Val Leu Arg Leu Ser Ala
                515   520   525

Ala Thr Gln Asp Leu Pro Lys Ser Val Val Cys Asn Val His Gly Val
                530   535   540

Asn Pro Lys Phe Leu Met Ile Gly Glu Lys Ile Ala Glu Glu Arg Ser
545   550   555   560

Arg Gly Glu Gln Ala Phe Ser Lys Gly Ala Tyr Phe Leu Gly Lys Met
                565   570   575

Val Trp Ala Lys Gly Tyr Arg Glu Leu Ile Asp Leu Met Ala Lys His
                580   585   590

Lys Ser Glu Leu Gly Ser Phe Asn Leu Asp Val Tyr Gly Asn Gly Glu
                595   600   605

Asp Ala Val Glu Val Gln Arg Ala Ala Lys Lys His Asp Leu Asn Leu

                                  103

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                    610                      615                        620

Asn Phe Leu Lys Gly Arg Asp His Ala Asp Asp Ala Leu His Lys Tyr
625                     630                 635                       640


Lys Val Phe Ile Asn Pro Ser Ile Ser Asp Val Leu Cys Thr Ala Thr
                    645                 650                       655


Ala Glu Ala Leu Ala Met Gly Lys Phe Val Val Cys Ala Asp His Pro
                660                 665                   670


Ser Asn Glu Phe Phe Arg Ser Phe Pro Asn Cys Leu Thr Tyr Lys Thr
            675                 680                   685


Ser Glu Asp Phe Val Ser Lys Val Gln Glu Ala Met Thr Lys Glu Pro
            690                 695                 700


Leu Pro Leu Thr Pro Glu Gln Met Tyr Asn Leu Ser Trp Glu Ala Ala
705                     710                 715                       720


Thr Gln Arg Phe Met Glu Tyr Ser Asp Leu Asp Lys Ile Leu Asn Asn
                    725                 730                   735


Gly Glu Gly Gly Arg Lys Met Arg Lys Ser Arg Ser Val Pro Ser Phe
                    740                 745                   750


Asn Glu Val Val Asp Gly Gly Leu Ala Phe Ser His Tyr Val Leu Thr
            755                 760                   765


Gly Asn Asp Phe Leu Arg Leu Cys Thr Gly Ala Thr Pro Arg Thr Lys
    770                 775                 780


Asp Tyr Asp Asn Gln His Cys Lys Asp Leu Asn Leu Val Pro Pro His
785                 790                 795                       800


Val His Lys Pro Ile Phe Gly Trp
                    805
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<210> 43

<211> 1299

<212> DNA

<213> Arabidopsis thaliana

104

<220>

<221> CDS

<222>   (1)..(1299)

<223>   23915

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Met Gly Ala Arg Val Gln Val Gln His Tyr Asn Leu Gly Ser Ser Asp
1               5                   10                  15

tcc tac atc gct act tct ctc cac gat ctc aac tcc gtc gat ggt ccg      96
Ser Tyr Ile Ala Thr Ser Leu His Asp Leu Asn Ser Val Asp Gly Pro
                20                  25                  30

ccg aga gat atc gac ggt atc gga ggc gcc gtt ggt cgt gac ggc gat     144
Pro Arg Asp Ile Asp Gly Ile Gly Gly Ala Val Gly Arg Asp Gly Asp
            35                  40                  45

agt tta gat aat gac ggc gat tcc tct tct gcg gac tgt atg cat gaa     192
Ser Leu Asp Asn Asp Gly Asp Ser Ser Ser Ala Asp Cys Met His Glu
        50                  55                  60

tca tac aga aac tct atg caa atc gga gta gaa gaa ggt gga tct aac     240
Ser Tyr Arg Asn Ser Met Gln Ile Gly Val Glu Glu Gly Gly Ser Asn
65                  70                  75                  80

atg gag aac aaa gga tct gct tac att atg tta aac att gaa gat gtt     288
Met Glu Asn Lys Gly Ser Ala Tyr Ile Met Leu Asn Ile Glu Asp Val
                85                  90                  95

tca ccg att gaa gca gca aga ggg agg ttt ctg caa atc ata ttg gac     336
Ser Pro Ile Glu Ala Ala Arg Gly Arg Phe Leu Gln Ile Ile Leu Asp
            100                 105                 110

tac ttt att agc caa cat gtg att gaa gtc tgt gag agc aaa cgt gat     384
Tyr Phe Ile Ser Gln His Val Ile Glu Val Cys Glu Ser Lys Arg Asp
        115                 120                 125

cat gat gtg gat tca gga gga cgt gat agt aat agt aaa gtg aag agg     432
His Asp Val Asp Ser Gly Gly Arg Asp Ser Asn Ser Lys Val Lys Arg
        130                 135                 140

aag tcg gat gat acg cga tat gaa ggt gat ccg agt ttt gcg tta ccg     480
Lys Ser Asp Asp Thr Arg Tyr Glu Gly Asp Pro Ser Phe Ala Leu Pro
145                 150                 155                 160

ttg atg tat att gca aat ttg tat gag act tta gtt ggt gaa gca aat     528
Leu Met Tyr Ile Ala Asn Leu Tyr Glu Thr Leu Val Gly Glu Ala Asn
                165                 170                 175

gtg agg ctt gct tca ttg aat gga ata agg gat aag act att gga gta     576
Val Arg Leu Ala Ser Leu Asn Gly Ile Arg Asp Lys Thr Ile Gly Val
            180                 185                 190
```

```
gct ctt gaa gct gct ggt ggc ttg tat agg aaa tta act aag aag ttt          624
Ala Leu Glu Ala Ala Gly Gly Leu Tyr Arg Lys Leu Thr Lys Lys Phe
            195                 200             205

cct aag aaa ggt act tgc atg tac agg aga aga gaa ctg gca act tca          672
Pro Lys Lys Gly Thr Cys Met Tyr Arg Arg Arg Glu Leu Ala Thr Ser
    210                 215                 220

gtt gaa aca agg aca aga ttt cca gaa ttg gta ata cat gaa gag aaa          720
Val Glu Thr Arg Thr Arg Phe Pro Glu Leu Val Ile His Glu Glu Lys
225                 230                 235                 240

cga gtt cgc ttt gtg gtg gtt aat ggt ttg gat att gtt gaa aag cca          768
Arg Val Arg Phe Val Val Val Asn Gly Leu Asp Ile Val Glu Lys Pro
                245                 250                 255

agt gat ttg cct att gaa gaa gct gaa tgg ttt aag cga tta aca ggc          816
Ser Asp Leu Pro Ile Glu Glu Ala Glu Trp Phe Lys Arg Leu Thr Gly
            260                 265                 270

cgt aat gaa gtg gct atc tct gct aga gat tat aaa ttc tac tgc cct          864
Arg Asn Glu Val Ala Ile Ser Ala Arg Asp Tyr Lys Phe Tyr Cys Pro
            275                 280                 285

cga cgc aag cat agg cgt ctt cag aat tct gtc tcc agc atc aat ggc          912
Arg Arg Lys His Arg Arg Leu Gln Asn Ser Val Ser Ser Ile Asn Gly
    290                 295                 300

ttg cct aca ttt cca ggt ata gac tct tca acg tta gct aat aca caa          960
Leu Pro Thr Phe Pro Gly Ile Asp Ser Ser Thr Leu Ala Asn Thr Gln
305                 310                 315                 320

gga ttt cgc gaa gat caa agc caa caa caa cac act cct tct cct tcc         1008
Gly Phe Arg Glu Asp Gln Ser Gln Gln Gln His Thr Pro Ser Pro Ser
                325                 330                 335

aaa cat cat atg tca tct ttg tct cat caa ttt cat caa tct att cac         1056
Lys His His Met Ser Ser Leu Ser His Gln Phe His Gln Ser Ile His
                340                 345                 350

cag agc cac caa cac cat caa tct ata tac caa agt caa cac gca gcc         1104
Gln Ser His Gln His His Gln Ser Ile Tyr Gln Ser Gln His Ala Ala
            355                 360                 365

aca cac tat ccc agt cag aac cat caa tgt gac cct gaa cta tct cac         1152
Thr His Tyr Pro Ser Gln Asn His Gln Cys Asp Pro Glu Leu Ser His
    370                 375                 380

aca caa atg gct tgc ttg caa ccc ctc act gga ggc cat gta atg cca         1200
Thr Gln Met Ala Cys Leu Gln Pro Leu Thr Gly Gly His Val Met Pro
385                 390                 395                 400

aat agt ccg gcg aaa ttt tgt gac caa tgt gga gca cag tac ttg aga         1248
Asn Ser Pro Ala Lys Phe Cys Asp Gln Cys Gly Ala Gln Tyr Leu Arg
                405                 410                 415

gag aca tcc aaa ttc tgc tca gag tgt ggt tcc aag aga ctc ggg ata         1296
Glu Thr Ser Lys Phe Cys Ser Glu Cys Gly Ser Lys Arg Leu Gly Ile
                420                 425                 430
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106

tag

<210> 44

<211> 432

<212> PRT

<213> Arabidopsis thaliana

<400> 44

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Met Gly Ala Arg Val Gln Val Gln His Tyr Asn Leu Gly Ser Ser Asp
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Ser Tyr Ile Ala Thr Ser Leu His Asp Leu Asn Ser Val Asp Gly Pro
            20                  25                  30


Pro Arg Asp Ile Asp Gly Ile Gly Gly Ala Val Gly Arg Asp Gly Asp
        35                  40                  45


Ser Leu Asp Asn Asp Gly Asp Ser Ser Ser Ala Asp Cys Met His Glu
    50                  55                  60


Ser Tyr Arg Asn Ser Met Gln Ile Gly Val Glu Glu Gly Gly Ser Asn
65                  70                  75                  80


Met Glu Asn Lys Gly Ser Ala Tyr Ile Met Leu Asn Ile Glu Asp Val
                85                  90                  95


Ser Pro Ile Glu Ala Ala Arg Gly Arg Phe Leu Gln Ile Ile Leu Asp
            100                 105                 110


Tyr Phe Ile Ser Gln His Val Ile Glu Val Cys Glu Ser Lys Arg Asp
        115                 120                 125


His Asp Val Asp Ser Gly Gly Arg Asp Ser Asn Ser Lys Val Lys Arg
    130                 135                 140


Lys Ser Asp Asp Thr Arg Tyr Glu Gly Asp Pro Ser Phe Ala Leu Pro
145                 150                 155                 160


Leu Met Tyr Ile Ala Asn Leu Tyr Glu Thr Leu Val Gly Glu Ala Asn
                165                 170                 175
```

```
Val Arg Leu Ala Ser Leu Asn Gly Ile Arg Asp Lys Thr Ile Gly Val
        180                 185                 190

Ala Leu Glu Ala Ala Gly Gly Leu Tyr Arg Lys Leu Thr Lys Lys Phe
        195                 200                 205

Pro Lys Lys Gly Thr Cys Met Tyr Arg Arg Arg Glu Leu Ala Thr Ser
    210                 215                 220

Val Glu Thr Arg Thr Arg Phe Pro Glu Leu Val Ile His Glu Glu Lys
225                 230                 235                 240

Arg Val Arg Phe Val Val Val Asn Gly Leu Asp Ile Val Glu Lys Pro
                245                 250                 255

Ser Asp Leu Pro Ile Glu Glu Ala Glu Trp Phe Lys Arg Leu Thr Gly
        260                 265                 270

Arg Asn Glu Val Ala Ile Ser Ala Arg Asp Tyr Lys Phe Tyr Cys Pro
        275                 280                 285

Arg Arg Lys His Arg Arg Leu Gln Asn Ser Val Ser Ser Ile Asn Gly
    290                 295                 300

Leu Pro Thr Phe Pro Gly Ile Asp Ser Ser Thr Leu Ala Asn Thr Gln
305                 310                 315                 320

Gly Phe Arg Glu Asp Gln Ser Gln Gln Gln His Thr Pro Ser Pro Ser
            325                 330                 335

Lys His His Met Ser Ser Leu Ser His Gln Phe His Gln Ser Ile His
        340                 345                 350

Gln Ser His Gln His His Gln Ser Ile Tyr Gln Ser Gln His Ala Ala
        355                 360                 365

Thr His Tyr Pro Ser Gln Asn His Gln Cys Asp Pro Glu Leu Ser His
    370                 375                 380

Thr Gln Met Ala Cys Leu Gln Pro Leu Thr Gly Gly His Val Met Pro
385                 390                 395                 400

Asn Ser Pro Ala Lys Phe Cys Asp Gln Cys Gly Ala Gln Tyr Leu Arg
                405                 410                 415
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108

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Glu Thr Ser Lys Phe Cys Ser Glu Cys Gly Ser Lys Arg Leu Gly Ile
        420                 425             430
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<210> 45

<211> 1617

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1617)

<223> 30945


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Met Asn Glu Asp Lys Asn Pro Ala Arg Ala Ile Asp Leu Ala Ala Ser
1               5                  10                  15

aat agc atg tat tta cgt gag acc ata ctt tct agt gaa tct cct agt     96
Asn Ser Met Tyr Leu Arg Glu Thr Ile Leu Ser Ser Glu Ser Pro Ser
            20                  25                  30

ctc aac act cag aat atc tca gtg aca gtt gaa atg cca ccc atg ttg    144
Leu Asn Thr Gln Asn Ile Ser Val Thr Val Glu Met Pro Pro Met Leu
        35                  40                  45

aaa ccg ttg cat ggg cat ctt ctt aaa cac ttt att gtg ttt tca aat    192
Lys Pro Leu His Gly His Leu Leu Lys His Phe Ile Val Phe Ser Asn
    50                  55                  60

att gaa gac cag aac agt atc atc ata ata att cat gct act aac aat    240
Ile Glu Asp Gln Asn Ser Ile Ile Ile Ile Ile His Ala Thr Asn Asn
65                  70                  75                  80

tgt cta cag cgt tgc ccg tca gtt act aaa gaa cag tgg gca gtg cca    288
Cys Leu Gln Arg Cys Pro Ser Val Thr Lys Glu Gln Trp Ala Val Pro
                85                  90                  95

gcg att ttg tct tct ttg aaa atg gaa gaa aac ctt ttg gcc cag gaa    336
Ala Ile Leu Ser Ser Leu Lys Met Glu Glu Asn Leu Leu Ala Gln Glu
            100                 105                 110

agg gcc tgt gtg ttc ctc tcc ttg ttg ctg cat aac ttc tcc atg gtt    384
Arg Ala Cys Val Phe Leu Ser Leu Leu Leu His Asn Phe Ser Met Val
        115                 120                 125

cac aca aca aaa act ggg aat act ctg aat gtt gat tct ttc tcc tgc    432
His Thr Thr Lys Thr Gly Asn Thr Leu Asn Val Asp Ser Phe Ser Cys
        130                 135                 140
```

109

```
ttg gat tct ttc tca aag cat ata cgt ggt ggt atg gct gat act gaa        480
Leu Asp Ser Phe Ser Lys His Ile Arg Gly Gly Met Ala Asp Thr Glu
145             150                 155                 160

gct gga gtt atg ctt tct gga ttt tcg gaa gaa ctc ctt tgt ctt ctt        528
Ala Gly Val Met Leu Ser Gly Phe Ser Glu Glu Leu Leu Cys Leu Leu
                165                 170                 175

cag gac ctc ctt tct ggg cag cgg gta tta ttt tcg gtt aaa tcc tca        576
Gln Asp Leu Leu Ser Gly Gln Arg Val Leu Phe Ser Val Lys Ser Ser
            180                 185                 190

gaa aca tgt gaa tct gat tta agc atc cct gtc acc ctg aat gga gaa        624
Glu Thr Cys Glu Ser Asp Leu Ser Ile Pro Val Thr Leu Asn Gly Glu
            195                 200                 205

aat gta gct ctc gtc aac aaa atc gct cta act gat caa ttg gtg gcc        672
Asn Val Ala Leu Val Asn Lys Ile Ala Leu Thr Asp Gln Leu Val Ala
210                 215                 220

gga agc gct att ttg gcg gca ata tgt act gca ctt gat cgt att gga        720
Gly Ser Ala Ile Leu Ala Ala Ile Cys Thr Ala Leu Asp Arg Ile Gly
225                 230                 235                 240

tat atc tgc gaa gct tcc ttt gaa atc ctg cac aag tac agt cat gag        768
Tyr Ile Cys Glu Ala Ser Phe Glu Ile Leu His Lys Tyr Ser His Glu
                245                 250                 255

aaa acc tca gtg cta ctg acc att ctt cac gtt ttt gct tac att gct        816
Lys Thr Ser Val Leu Leu Thr Ile Leu His Val Phe Ala Tyr Ile Ala
                260                 265                 270

gga gag aaa atg gtg ttg tct agt gag cat ggc ata tca att gca gtg        864
Gly Glu Lys Met Val Leu Ser Ser Glu His Gly Ile Ser Ile Ala Val
            275                 280                 285

ttg aaa tac att gtc atg ttt cta gaa aac aaa cat ttt ggt act gtg        912
Leu Lys Tyr Ile Val Met Phe Leu Glu Asn Lys His Phe Gly Thr Val
            290                 295                 300

gag ggc agt tct cga ttg cac cca ggc aag aac aag tgt cca ttc tca        960
Glu Gly Ser Ser Arg Leu His Pro Gly Lys Asn Lys Cys Pro Phe Ser
305                 310                 315                 320

gac agg tct tcc tcg ctg gag gct atg gca tct aag ctc atg gaa att       1008
Asp Arg Ser Ser Ser Leu Glu Ala Met Ala Ser Lys Leu Met Glu Ile
                325                 330                 335

ctt cag gaa ttt act gag tct aat act ttg cat aaa agc ttg act ggt       1056
Leu Gln Glu Phe Thr Glu Ser Asn Thr Leu His Lys Ser Leu Thr Gly
                340                 345                 350

tca ttg ggt tct agc cac cta gag aag acc gag ttt agg ccg gca cac       1104
Ser Leu Gly Ser Ser His Leu Glu Lys Thr Glu Phe Arg Pro Ala His
            355                 360                 365

aaa gat ttc cag tgt gta ttg acc agg gat caa agt atc aat ctc tgt       1152
Lys Asp Phe Gln Cys Val Leu Thr Arg Asp Gln Ser Ile Asn Leu Cys
370                 375                 380
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110

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gac att cta tca ttg gtg gag ctt att gct tgt tat acg gct tgg gat      1200
Asp Ile Leu Ser Leu Val Glu Leu Ile Ala Cys Tyr Thr Ala Trp Asp
385                     390                 395                 400

tgg act agt gcg aac att gtt gct cca ctg ctt aag atg ctg gga atg      1248
Trp Thr Ser Ala Asn Ile Val Ala Pro Leu Leu Lys Met Leu Gly Met
                405                 410                 415

cca ttg cca atg aac ctc tct gtt gca atc gtc tcc ctt ctt ggg caa      1296
Pro Leu Pro Met Asn Leu Ser Val Ala Ile Val Ser Leu Leu Gly Gln
                420                 425                 430

ctt agc agt att gga gtg gat gct ggt ggc tat gaa aac gaa gga atc      1344
Leu Ser Ser Ile Gly Val Asp Ala Gly Gly Tyr Glu Asn Glu Gly Ile
                435                 440                 445

tca aac ttg aga gtg aaa ctg tca gca ttt cta cag tgt gag acg aca      1392
Ser Asn Leu Arg Val Lys Leu Ser Ala Phe Leu Gln Cys Glu Thr Thr
450                     455                 460

cta aag gcc ggt ttt gca gtg cag ata gca act gtg agc tcc ctc ctg      1440
Leu Lys Ala Gly Phe Ala Val Gln Ile Ala Thr Val Ser Ser Leu Leu
465                     470                 475                 480

aag acg ctg cag ctg aaa ttc cca ata gac ttt caa gac aaa acc acc      1488
Lys Thr Leu Gln Leu Lys Phe Pro Ile Asp Phe Gln Asp Lys Thr Thr
                485                 490                 495

atg att ccg ggt agt ggc gac caa agc tta tct ggt tca gtc aat gtg      1536
Met Ile Pro Gly Ser Gly Asp Gln Ser Leu Ser Gly Ser Val Asn Val
                500                 505                 510

gtg acc aag tgg ttg tcg ttg ttg agc aag gaa caa cga gtt ttc gca      1584
Val Thr Lys Trp Leu Ser Leu Leu Ser Lys Glu Gln Arg Val Phe Ala
                515                 520                 525

ttt gag ttt cta caa acc aat gtt gtt aga tga                          1617
Phe Glu Phe Leu Gln Thr Asn Val Val Arg
                530                 535
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<210> 46

<211> 538

<212> PRT

<213> Arabidopsis thaliana

<400> 46

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Met Asn Glu Asp Lys Asn Pro Ala Arg Ala Ile Asp Leu Ala Ala Ser
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Asn Ser Met Tyr Leu Arg Glu Thr Ile Leu Ser Ser Glu Ser Pro Ser
            20                  25                  30
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Leu Asn Thr Gln Asn Ile Ser Val Thr Val Glu Met Pro Pro Met Leu
        35   40   45

Lys Pro Leu His Gly His Leu Leu Lys His Phe Ile Val Phe Ser Asn
    50   55   60

Ile Glu Asp Gln Asn Ser Ile Ile Ile Ile His Ala Thr Asn Asn
65   70   75   80

Cys Leu Gln Arg Cys Pro Ser Val Thr Lys Glu Gln Trp Ala Val Pro
            85   90   95

Ala Ile Leu Ser Ser Leu Lys Met Glu Glu Asn Leu Leu Ala Gln Glu
            100   105   110

Arg Ala Cys Val Phe Leu Ser Leu Leu Leu His Asn Phe Ser Met Val
        115   120   125

His Thr Thr Lys Thr Gly Asn Thr Leu Asn Val Asp Ser Phe Ser Cys
    130   135   140

Leu Asp Ser Phe Ser Lys His Ile Arg Gly Gly Met Ala Asp Thr Glu
145   150   155   160

Ala Gly Val Met Leu Ser Gly Phe Ser Glu Glu Leu Leu Cys Leu Leu
            165   170   175

Gln Asp Leu Leu Ser Gly Gln Arg Val Leu Phe Ser Val Lys Ser Ser
        180   185   190

Glu Thr Cys Glu Ser Asp Leu Ser Ile Pro Val Thr Leu Asn Gly Glu
        195   200   205

Asn Val Ala Leu Val Asn Lys Ile Ala Leu Thr Asp Gln Leu Val Ala
    210   215   220

Gly Ser Ala Ile Leu Ala Ala Ile Cys Thr Ala Leu Asp Arg Ile Gly
225   230   235   240

Tyr Ile Cys Glu Ala Ser Phe Glu Ile Leu His Lys Tyr Ser His Glu
            245   250   255

Lys Thr Ser Val Leu Leu Thr Ile Leu His Val Phe Ala Tyr Ile Ala
        260   265   270

112

Gly Glu Lys Met Val Leu Ser Ser Glu His Gly Ile Ser Ile Ala Val
        275   280   285

Leu Lys Tyr Ile Val Met Phe Leu Glu Asn Lys His Phe Gly Thr Val
        290   295   300

Glu Gly Ser Ser Arg Leu His Pro Gly Lys Asn Lys Cys Pro Phe Ser
305   310   315   320

Asp Arg Ser Ser Ser Leu Glu Ala Met Ala Ser Lys Leu Met Glu Ile
                325   330   335

Leu Gln Glu Phe Thr Glu Ser Asn Thr Leu His Lys Ser Leu Thr Gly
            340   345   350

Ser Leu Gly Ser Ser His Leu Glu Lys Thr Glu Phe Arg Pro Ala His
        355   360   365

Lys Asp Phe Gln Cys Val Leu Thr Arg Asp Gln Ser Ile Asn Leu Cys
    370   375   380

Asp Ile Leu Ser Leu Val Glu Leu Ile Ala Cys Tyr Thr Ala Trp Asp
385   390   395   400

Trp Thr Ser Ala Asn Ile Val Ala Pro Leu Leu Lys Met Leu Gly Met
            405   410   415

Pro Leu Pro Met Asn Leu Ser Val Ala Ile Val Ser Leu Leu Gly Gln
        420   425   430

Leu Ser Ser Ile Gly Val Asp Ala Gly Gly Tyr Glu Asn Glu Gly Ile
        435   440   445

Ser Asn Leu Arg Val Lys Leu Ser Ala Phe Leu Gln Cys Glu Thr Thr
    450   455   460

Leu Lys Ala Gly Phe Ala Val Gln Ile Ala Thr Val Ser Ser Leu Leu
465   470   475   480

Lys Thr Leu Gln Leu Lys Phe Pro Ile Asp Phe Gln Asp Lys Thr Thr
            485   490   495

Met Ile Pro Gly Ser Gly Asp Gln Ser Leu Ser Gly Ser Val Asn Val
        500   505   510

113

Val Thr Lys Trp Leu Ser Leu Leu Ser Lys Glu Gln Arg Val Phe Ala
        515   520   525

Phe Glu Phe Leu Gln Thr Asn Val Val Arg
    530   535

<210> 47

<211> 1332

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1332)

<223> 31895

<400> 47
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Met Ser Ile Thr Tyr Ser Ala Ile Ser Ser Ser Thr Val Ser Gly Phe
1   5   10   15

tca cca aaa agt gta cct ttt gct att cat agc gta acc agg agg caa   96
Ser Pro Lys Ser Val Pro Phe Ala Ile His Ser Val Thr Arg Arg Gln
            20   25   30

ttt ctt aat ccc aac acg ttt tat aga ttt ggg ttc tct cct tct ctt   144
Phe Leu Asn Pro Asn Thr Phe Tyr Arg Phe Gly Phe Ser Pro Ser Leu
        35   40   45

cag gga agt agc att gag ttt agc ctt cag ttg aat tca aga gtt gtg   192
Gln Gly Ser Ser Ile Glu Phe Ser Leu Gln Leu Asn Ser Arg Val Val
    50   55   60

ctt agt aaa gag cgt cga tct ctg cca tta gtt gtg aga aat gat cgt   240
Leu Ser Lys Glu Arg Arg Ser Leu Pro Leu Val Val Arg Asn Asp Arg
65   70   75   80

cct cag aat gaa gac tta cct aag cag tac aca agg cga gag aag aaa   288
Pro Gln Asn Glu Asp Leu Pro Lys Gln Tyr Thr Arg Arg Glu Lys Lys
                85   90   95

cct ttc cca gtc cct att gtg gac ctg aga cga gct gcg agg gag aga   336
Pro Phe Pro Val Pro Ile Val Asp Leu Arg Arg Ala Ala Arg Glu Arg
            100   105   110

gtc aag aac aac aaa gac aaa cct aag aga cct cta cct ccg cct aaa   384

114

Val Lys Asn Asn Lys Asp Lys Pro Lys Arg Pro Leu Pro Pro Pro Lys
        115   120   125

aat ggt atg gtt gtg aag agc ctt gtg cct ctt gct tat aaa gta tac   432
Asn Gly Met Val Val Lys Ser Leu Val Pro Leu Ala Tyr Lys Val Tyr
        130   135   140

aat gca aga atc aga ttg atc aac aat ctc cac cgg ctt atg aaa gtt   480
Asn Ala Arg Ile Arg Leu Ile Asn Asn Leu His Arg Leu Met Lys Val
145   150   155   160

gtt cgt gtt aat gct tgt ggg tgg tgc aat gag att cat gtt gga cct   528
Val Arg Val Asn Ala Cys Gly Trp Cys Asn Glu Ile His Val Gly Pro
                165   170   175

tat ggg cat cca ttt aag tcg tgt aaa ggt ccc aat act tcc caa agg   576
Tyr Gly His Pro Phe Lys Ser Cys Lys Gly Pro Asn Thr Ser Gln Arg
                180   185   190

aaa ggt ctt cat gaa tgg act aac tcg gtt att gag gac gtt att gtt   624
Lys Gly Leu His Glu Trp Thr Asn Ser Val Ile Glu Asp Val Ile Val
        195   200   205

cct ctt gaa gcc tat cac ctt ttt gac cgc ctt ggc aag cgt atc cgt   672
Pro Leu Glu Ala Tyr His Leu Phe Asp Arg Leu Gly Lys Arg Ile Arg
        210   215   220

cat gat gaa aga ttc tcg att ccc cga gtt cct gct gta gtt gag ctc   720
His Asp Glu Arg Phe Ser Ile Pro Arg Val Pro Ala Val Val Glu Leu
225   230   235   240

tgc att cag ggc ggc gtt gaa ata ccc gaa ttt cca gca aaa agg aga   768
Cys Ile Gln Gly Gly Val Glu Ile Pro Glu Phe Pro Ala Lys Arg Arg
                245   250   255

aga aaa ccg att atc cgc att ggc aaa agc gag ttt gtt gat gca gat   816
Arg Lys Pro Ile Ile Arg Ile Gly Lys Ser Glu Phe Val Asp Ala Asp
                260   265   270

gaa act gaa ttg cct gat cca gag cct cag cct cct cca gtg cca ttg   864
Glu Thr Glu Leu Pro Asp Pro Glu Pro Gln Pro Pro Pro Val Pro Leu
        275   280   285

tta act gag tta cct gtc tca gag atc act ccc cca tct agc gaa gaa   912
Leu Thr Glu Leu Pro Val Ser Glu Ile Thr Pro Pro Ser Ser Glu Glu
        290   295   300

gaa aca gtc tcc tta gcc gaa gaa aca tta cag gcc tgg gaa gaa atg   960
Glu Thr Val Ser Leu Ala Glu Glu Thr Leu Gln Ala Trp Glu Glu Met
305   310   315   320

aga gca gga gcc aaa aag ctg atg agg atg tac agg gtt agg gtc tgt   1008
Arg Ala Gly Ala Lys Lys Leu Met Arg Met Tyr Arg Val Arg Val Cys
                325   330   335

ggg tac tgt cca gag gtt cac gta ggt cca acg gga cac aag gcc cag   1056
Gly Tyr Cys Pro Glu Val His Val Gly Pro Thr Gly His Lys Ala Gln
                340   345   350

aac tgt ggt gca ttc aag cac caa cag cgg aat ggc cag cat ggt tgg   1104

115

```
Asn Cys Gly Ala Phe Lys His Gln Gln Arg Asn Gly Gln His Gly Trp
        355             360             365

caa tct gca gta ctt gac gac ttg ata ccg cca aga tat gtt tgg cat      1152
Gln Ser Ala Val Leu Asp Asp Leu Ile Pro Pro Arg Tyr Val Trp His
        370             375             380

gtt cct gat gtg aat ggg cca ccg atg cag cga gag cta cga agc ttc      1200
Val Pro Asp Val Asn Gly Pro Pro Met Gln Arg Glu Leu Arg Ser Phe
385             390             395             400

tac ggg caa gca cct gct gtt gtg gag ata tgt gct cag gct ggc gct      1248
Tyr Gly Gln Ala Pro Ala Val Val Glu Ile Cys Ala Gln Ala Gly Ala
                405             410             415

gtt gta cct gag cat tat aga gct aca atg aga ctg gag gtt gga att      1296
Val Val Pro Glu His Tyr Arg Ala Thr Met Arg Leu Glu Val Gly Ile
            420             425             430

cct tcg agt gtg aaa gaa gct gag atg gtt gtt tga                      1332
Pro Ser Ser Val Lys Glu Ala Glu Met Val Val
        435             440
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<210> 48

<211> 443

<212> PRT

<213> Arabidopsis thaliana

<400> 48

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Met Ser Ile Thr Tyr Ser Ala Ile Ser Ser Ser Thr Val Ser Gly Phe
1               5               10              15


Ser Pro Lys Ser Val Pro Phe Ala Ile His Ser Val Thr Arg Arg Gln
            20              25              30


Phe Leu Asn Pro Asn Thr Phe Tyr Arg Phe Gly Phe Ser Pro Ser Leu
        35              40              45


Gln Gly Ser Ser Ile Glu Phe Ser Leu Gln Leu Asn Ser Arg Val Val
    50              55              60


Leu Ser Lys Glu Arg Arg Ser Leu Pro Leu Val Val Arg Asn Asp Arg
65              70              75              80


Pro Gln Asn Glu Asp Leu Pro Lys Gln Tyr Thr Arg Arg Glu Lys Lys
                85              90              95
```

116

Pro Phe Pro Val Pro Ile Val Asp Leu Arg Arg Ala Ala Arg Glu Arg
            100   105   110

Val Lys Asn Asn Lys Asp Lys Pro Lys Arg Pro Leu Pro Pro Pro Lys
            115   120   125

Asn Gly Met Val Val Lys Ser Leu Val Pro Leu Ala Tyr Lys Val Tyr
            130   135   140

Asn Ala Arg Ile Arg Leu Ile Asn Asn Leu His Arg Leu Met Lys Val
145   150   155   160

Val Arg Val Asn Ala Cys Gly Trp Cys Asn Glu Ile His Val Gly Pro
                165   170   175

Tyr Gly His Pro Phe Lys Ser Cys Lys Gly Pro Asn Thr Ser Gln Arg
                180   185   190

Lys Gly Leu His Glu Trp Thr Asn Ser Val Ile Glu Asp Val Ile Val
            195   200   205

Pro Leu Glu Ala Tyr His Leu Phe Asp Arg Leu Gly Lys Arg Ile Arg
    210   215   220

His Asp Glu Arg Phe Ser Ile Pro Arg Val Pro Ala Val Val Glu Leu
225   230   235   240

Cys Ile Gln Gly Gly Val Glu Ile Pro Glu Phe Pro Ala Lys Arg Arg
                245   250   255

Arg Lys Pro Ile Ile Arg Ile Gly Lys Ser Glu Phe Val Asp Ala Asp
            260   265   270

Glu Thr Glu Leu Pro Asp Pro Glu Pro Gln Pro Pro Val Pro Leu
    275   280   285

Leu Thr Glu Leu Pro Val Ser Glu Ile Thr Pro Pro Ser Ser Glu Glu
    290   295   300

Glu Thr Val Ser Leu Ala Glu Glu Thr Leu Gln Ala Trp Glu Glu Met
305   310   315   320

Arg Ala Gly Ala Lys Lys Leu Met Arg Met Tyr Arg Val Arg Val Cys
                325   330   335

117

```
Gly Tyr Cys Pro Glu Val His Val Gly Pro Thr Gly His Lys Ala Gln
            340                 345                 350


Asn Cys Gly Ala Phe Lys His Gln Gln Arg Asn Gly Gln His Gly Trp
            355                 360                 365


Gln Ser Ala Val Leu Asp Asp Leu Ile Pro Pro Arg Tyr Val Trp His
            370                 375                 380


Val Pro Asp Val Asn Gly Pro Pro Met Gln Arg Glu Leu Arg Ser Phe
385                 390                 395                 400


Tyr Gly Gln Ala Pro Ala Val Val Glu Ile Cys Ala Gln Ala Gly Ala
                405                 410                 415


Val Val Pro Glu His Tyr Arg Ala Thr Met Arg Leu Glu Val Gly Ile
            420                 425                 430


Pro Ser Ser Val Lys Glu Ala Glu Met Val Val
            435                 440
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<210> 49

<211> 540

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(540)

<223> 34269


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<400> 49
atg tta tca agc att gtt gtt gtt gtc acc agg atc gaa aat ttt caa      48
Met Leu Ser Ser Ile Val Val Val Val Thr Arg Ile Glu Asn Phe Gln
1               5                   10                  15

tgt tgt tgt ttg aga gag atg atg gct gcg aag ctt cag aaa tgg cga      96
Cys Cys Cys Leu Arg Glu Met Met Ala Ala Lys Leu Gln Lys Trp Arg
            20                  25                  30

aat ctg gca ggt cgt cta gat ctg atg aat cgg agc ggc gct gtg tcg     144
Asn Leu Ala Gly Arg Leu Asp Leu Met Asn Arg Ser Gly Ala Val Ser
            35                  40                  45
```

```
acg agg cgg ttc ctg cac gaa ggt cca gat acc gtg gag gag ctt ctc          192
Thr Arg Arg Phe Leu His Glu Gly Pro Asp Thr Val Glu Glu Leu Leu
    50                  55                  60

gaa aga cat cta gcg aag aaa gag aaa cca ata atc gat cac gat gag          240
Glu Arg His Leu Ala Lys Lys Glu Lys Pro Ile Ile Asp His Asp Glu
65                  70                  75                  80

gct gag ttt ctg aat aga cgg cgt ctg acg agc acg cgc cgg gaa gcg          288
Ala Glu Phe Leu Asn Arg Arg Arg Leu Thr Ser Thr Arg Arg Glu Ala
                    85                  90                  95

ttg agt ttg tac aga gac ata tta cga gcg act cgg ttc ttc acg tgg          336
Leu Ser Leu Tyr Arg Asp Ile Leu Arg Ala Thr Arg Phe Phe Thr Trp
                100                 105                 110

att gat tcc agg gga aat tta tgg agg gac gtg ttg aga gag aac gcg          384
Ile Asp Ser Arg Gly Asn Leu Trp Arg Asp Val Leu Arg Glu Asn Ala
                115                 120                 125

agg aag gag ttt gaa gcg gcg cga ttt gag acg gat ccg gag gtt atc          432
Arg Lys Glu Phe Glu Ala Ala Arg Phe Glu Thr Asp Pro Glu Val Ile
    130                 135                 140

aca agg ctt ctg ata ggt gga agc gac gcc gtt tcg tct gct tta gat          480
Thr Arg Leu Leu Ile Gly Gly Ser Asp Ala Val Ser Ser Ala Leu Asp
145                 150                 155                 160

aag ctt gcg gag aag caa aga gag atg att gag aaa caa cgc cgt ggt          528
Lys Leu Ala Glu Lys Gln Arg Glu Met Ile Glu Lys Gln Arg Arg Gly
                165                 170                 175

gat caa cgc tga                                                          540
Asp Gln Arg
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<210> 50

<211> 179

<212> PRT

<213> Arabidopsis thaliana

<400> 50

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Met Leu Ser Ser Ile Val Val Val Val Thr Arg Ile Glu Asn Phe Gln
1                   5                   10                  15


Cys Cys Cys Leu Arg Glu Met Met Ala Ala Lys Leu Gln Lys Trp Arg
                20                  25                  30


Asn Leu Ala Gly Arg Leu Asp Leu Met Asn Arg Ser Gly Ala Val Ser
        35                  40                  45
```

119

Thr Arg Arg Phe Leu His Glu Gly Pro Asp Thr Val Glu Glu Leu Leu
    50   55   60

Glu Arg His Leu Ala Lys Lys Glu Lys Pro Ile Ile Asp His Asp Glu
65   70   -   75   80

Ala Glu Phe Leu Asn Arg Arg Arg Leu Thr Ser Thr Arg Arg Glu Ala
                85   90   95

Leu Ser Leu Tyr Arg Asp Ile Leu Arg Ala Thr Arg Phe Phe Thr Trp
            100   105   110

Ile Asp Ser Arg Gly Asn Leu Trp Arg Asp Val Leu Arg Glu Asn Ala
            115   120   125

Arg Lys Glu Phe Glu Ala Ala Arg Phe Glu Thr Asp Pro Glu Val Ile
    130   135   140

Thr Arg Leu Leu Ile Gly Gly Ser Asp Ala Val Ser Ser Ala Leu Asp
145   150   155   160

Lys Leu Ala Glu Lys Gln Arg Glu Met Ile Glu Lys Gln Arg Arg Gly
            165   170   175

Asp Gln Arg

<210>   51

<211>   708

<212>   DNA

<213>   Arabidopsis thaliana

<220>

<221>   CDS

<222>   (1)..(708)

<223>   34540

<400>   51
atg aga tcc cct aga acc ttg gag gtt tgg aag cta ggc act gtc aac   48

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Met Arg Ser Pro Arg Thr Leu Glu Val Trp Lys Leu Gly Thr Val Asn
1                 5                   10                  15

tat ttg aaa tcc ctt aaa ctg cag gag aaa tta gtt tca gag aga aaa      96
Tyr Leu Lys Ser Leu Lys Leu Gln Glu Lys Leu Val Ser Glu Arg Lys
                20                  25                  30

gct cat cag att cca gat acc ctc ctc tcg ctt cag cat cca cca act     144
Ala His Gln Ile Pro Asp Thr Leu Leu Ser Leu Gln His Pro Pro Thr
            35                  40                  45

tat acg ctc gga aag cgt aga acc gat cac aat cta ctt atc cct gaa     192
Tyr Thr Leu Gly Lys Arg Arg Thr Asp His Asn Leu Leu Ile Pro Glu
        50                  55                  60

tct gaa ctt aca aaa atc gga gct gaa ctt cat tat act caa aga gga     240
Ser Glu Leu Thr Lys Ile Gly Ala Glu Leu His Tyr Thr Gln Arg Gly
65                  70                  75                  80

gga gac atc acc ttc cat ggc cct cat caa gcc atc tta tat ccc atc     288
Gly Asp Ile Thr Phe His Gly Pro His Gln Ala Ile Leu Tyr Pro Ile
                85                  90                  95

att tcc tta cgc agc att ggt ttt ggt gct agg aac tac gtg gag aca     336
Ile Ser Leu Arg Ser Ile Gly Phe Gly Ala Arg Asn Tyr Val Glu Thr
            100                 105                 110

ttg gag cgg tca atg atc gag ttt gct tcg att tat ggc gtg aaa gct     384
Leu Glu Arg Ser Met Ile Glu Phe Ala Ser Ile Tyr Gly Val Lys Ala
        115                 120                 125

cga gca gga aac aaa tgt gag act ggg gtt tgg gtt ggg gat agg aag     432
Arg Ala Gly Asn Lys Cys Glu Thr Gly Val Trp Val Gly Asp Arg Lys
    130                 135                 140

atc ggt gct att ggg gtt agg ata tct tct gga atc act agt cat ggt     480
Ile Gly Ala Ile Gly Val Arg Ile Ser Ser Gly Ile Thr Ser His Gly
145                 150                 155                 160

ttg gcc tta aat ata gat cct gat atg aag tac ttt gag cac att gtg     528
Leu Ala Leu Asn Ile Asp Pro Asp Met Lys Tyr Phe Glu His Ile Val
                165                 170                 175

cct tgt ggg att gct gat aaa gaa gtt aca tct ttg cga aga gag acg     576
Pro Cys Gly Ile Ala Asp Lys Glu Val Thr Ser Leu Arg Arg Glu Thr
            180                 185                 190

gat act ctg ctt cct tca gaa gaa gtg att cat gaa cag ttg gtt tct     624
Asp Thr Leu Leu Pro Ser Glu Glu Val Ile His Glu Gln Leu Val Ser
        195                 200                 205

tgt tta gcc aaa gcg ttt tct tat gat gat gtt gtc tgg aag gaa gat     672
Cys Leu Ala Lys Ala Phe Ser Tyr Asp Asp Val Val Trp Lys Glu Asp
    210                 215                 220

cct tca ctc att ttg gac acc caa gat aaa gaa taa                     708
Pro Ser Leu Ile Leu Asp Thr Gln Asp Lys Glu
225                 230                 235
```

121

<210> 52

<211> 235

<212> PRT

<213> Arabidopsis thaliana

<400> 52

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Met Arg Ser Pro Arg Thr Leu Glu Val Trp Lys Leu Gly Thr Val Asn
1               5                   10                  15

Tyr Leu Lys Ser Leu Lys Leu Gln Glu Lys Leu Val Ser Glu Arg Lys
            20                  25                  30

Ala His Gln Ile Pro Asp Thr Leu Leu Ser Leu Gln His Pro Pro Thr
        35                  40                  45

Tyr Thr Leu Gly Lys Arg Arg Thr Asp His Asn Leu Leu Ile Pro Glu
    50                  55                  60

Ser Glu Leu Thr Lys Ile Gly Ala Glu Leu His Tyr Thr Gln Arg Gly
65                  70                  75                  80

Gly Asp Ile Thr Phe His Gly Pro His Gln Ala Ile Leu Tyr Pro Ile
                85                  90                  95

Ile Ser Leu Arg Ser Ile Gly Phe Gly Ala Arg Asn Tyr Val Glu Thr
            100                 105                 110

Leu Glu Arg Ser Met Ile Glu Phe Ala Ser Ile Tyr Gly Val Lys Ala
        115                 120                 125

Arg Ala Gly Asn Lys Cys Glu Thr Gly Val Trp Val Gly Asp Arg Lys
    130                 135                 140

Ile Gly Ala Ile Gly Val Arg Ile Ser Ser Gly Ile Thr Ser His Gly
145                 150                 155                 160

Leu Ala Leu Asn Ile Asp Pro Asp Met Lys Tyr Phe Glu His Ile Val
                165                 170                 175

Pro Cys Gly Ile Ala Asp Lys Glu Val Thr Ser Leu Arg Arg Glu Thr
            180                 185                 190
```

122

```
Asp Thr Leu Leu Pro Ser Glu Glu Val Ile His Glu Gln Leu Val Ser
         195                 200                 205


Cys Leu Ala Lys Ala Phe Ser Tyr Asp Asp Val Val Trp Lys Glu Asp
     210                 215                 220


Pro Ser Leu Ile Leu Asp Thr Gln Asp Lys Glu
225                 230                 235
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<210> 53

<211> 1473

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1473)

<223>


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<400>  53
atg cag aca ttt tca att tca ctc ctc cgt cac tct tct ccg ttc ctc      48
Met Gln Thr Phe Ser Ile Ser Leu Leu Arg His Ser Ser Pro Phe Leu
1                 5                   10                  15


cgt cac acc gcg att ttt cac ggc gga gtt gga gtt aga ttc aaa ttc      96
Arg His Thr Ala Ile Phe His Gly Gly Val Gly Val Arg Phe Lys Phe
                 20                  25                  30


ctt cgc agc ttt tct cct ctc tca gca aga cga gat aat ccc gat gtc     144
Leu Arg Ser Phe Ser Pro Leu Ser Ala Arg Arg Asp Asn Pro Asp Val
                 35                  40                  45


tcc aga aaa ccc caa ccg agc aaa aat atg ctc aga gcg aag cac atc     192
Ser Arg Lys Pro Gln Pro Ser Lys Asn Met Leu Arg Ala Lys His Ile
         50                  55                  60


ggt aaa aat tac tcc tcc tcc ttg tca cca gtt ctc tcg ccg gag cat     240
Gly Lys Asn Tyr Ser Ser Ser Leu Ser Pro Val Leu Ser Pro Glu His
65                  70                  75                  80


aaa cct tcg ctc tta gag tct caa gct att ggt act gtc gca aca gct     288
Lys Pro Ser Leu Leu Glu Ser Gln Ala Ile Gly Thr Val Ala Thr Ala
                 85                  90                  95


caa gcg aac ttt atg cgc gtc att gtt caa gat gta gct aat tct gtg     336
Gln Ala Asn Phe Met Arg Val Ile Val Gln Asp Val Ala Asn Ser Val
                 100                 105                 110
```

```
acg agt gat gat gat aat gat tct tca aag act ggt gtt gaa ttg ctt      384
Thr Ser Asp Asp Asp Asn Asp Ser Ser Lys Thr Gly Val Glu Leu Leu
        115                 120                 125

tgt gtg gtg aga gct gtg ttg aag aaa ata cga agg aga gtt tta gtt      432
Cys Val Val Arg Ala Val Leu Lys Lys Ile Arg Arg Arg Val Leu Val
    130                 135                 140

gga gat aag gtt ctt gtt gga tct att gat tgg gtt gat aga aga gga      480
Gly Asp Lys Val Leu Val Gly Ser Ile Asp Trp Val Asp Arg Arg Gly
145                 150                 155                 160

atg att gag aat gtg ttt cat cga cgt tcg gag att ttg gat cca cct      528
Met Ile Glu Asn Val Phe His Arg Arg Ser Glu Ile Leu Asp Pro Pro
                165                 170                 175

gtt gcg aac gtt gat cat ttg ctt gtt ctt ttc tct ttg gat caa ccg      576
Val Ala Asn Val Asp His Leu Leu Val Leu Phe Ser Leu Asp Gln Pro
                180                 185                 190

aaa ctt gag ccg ttt act ctt act agg ttc ttg gtg gaa gct gaa tct      624
Lys Leu Glu Pro Phe Thr Leu Thr Arg Phe Leu Val Glu Ala Glu Ser
            195                 200                 205

act cgt att cca tta aca ctt gct ttg aat aaa act gaa ctc att agt      672
Thr Arg Ile Pro Leu Thr Leu Ala Leu Asn Lys Thr Glu Leu Ile Ser
    210                 215                 220

gaa gag gaa ttg gaa act tgg aag ata agg ttg cgt gga tgg aac tat      720
Glu Glu Glu Leu Glu Thr Trp Lys Ile Arg Leu Arg Gly Trp Asn Tyr
225                 230                 235                 240

gaa cca ttg ttt tgt agt gtg gga act aaa gat gga ctt gat gat att      768
Glu Pro Leu Phe Cys Ser Val Gly Thr Lys Asp Gly Leu Asp Asp Ile
                245                 250                 255

gcg ttt gtt ctg aga gat cag act tct gtg att gtt gga cct agt ggt      816
Ala Phe Val Leu Arg Asp Gln Thr Ser Val Ile Val Gly Pro Ser Gly
                260                 265                 270

gtt gga aag tcg agt tta atc aac gta ttg agg agt aat cat ggt ggt      864
Val Gly Lys Ser Ser Leu Ile Asn Val Leu Arg Ser Asn His Gly Gly
            275                 280                 285

ggt gtg gtg gaa gat gag aat tgg ttt gag cct atg tta ggt aat aag      912
Gly Val Val Glu Asp Glu Asn Trp Phe Glu Pro Met Leu Gly Asn Lys
    290                 295                 300

tgg ttt gat gat cag cga gta ggg gaa gtt tcg agt aga agt ggt aga      960
Trp Phe Asp Asp Gln Arg Val Gly Glu Val Ser Ser Arg Ser Gly Arg
305                 310                 315                 320

ggt aaa cat aca aca cga aat gta tcg cta ctg ccg gtt tct gaa ggt      1008
Gly Lys His Thr Thr Arg Asn Val Ser Leu Leu Pro Val Ser Glu Gly
                325                 330                 335

ggt tac ctc gct gat act cct ggc ttt aac cag cct agt ttg ctg aaa      1056
Gly Tyr Leu Ala Asp Thr Pro Gly Phe Asn Gln Pro Ser Leu Leu Lys
            340                 345                 350
```

124

```
gta acg aag cat tca cta gct cac tgt ttt cct gag ata cgg aac atg     1104
Val Thr Lys His Ser Leu Ala His Cys Phe Pro Glu Ile Arg Asn Met
        355                 360                 365

att gag agc gaa aaa tgt gga ttc aga gac tgc ttg cat att ggg gaa     1152
Ile Glu Ser Glu Lys Cys Gly Phe Arg Asp Cys Leu His Ile Gly Glu
        370                 375                 380

cca gga tgt gtt gtg aaa ggt gac tgg gaa agg tat cct tac tac tta     1200
Pro Gly Cys Val Val Lys Gly Asp Trp Glu Arg Tyr Pro Tyr Tyr Leu
385                 390                 395                 400

caa ttg ctt gat gag atc aga atc agg gaa gaa ttt cag ctt agg act     1248
Gln Leu Leu Asp Glu Ile Arg Ile Arg Glu Glu Phe Gln Leu Arg Thr
                405                 410                 415

ttt gga acc aaa agg gaa gat gat gtt agg tac aag gtg gga gac atg     1296
Phe Gly Thr Lys Arg Glu Asp Asp Val Arg Tyr Lys Val Gly Asp Met
                420                 425                 430

ggt gtg aaa cat gct gaa cca cgg tta atg cct aag aag cat agg aga     1344
Gly Val Lys His Ala Glu Pro Arg Leu Met Pro Lys Lys His Arg Arg
                435                 440                 445

gag tca agg aag aaa acg aaa cag aca atg atc agt gag ctg gat gag     1392
Glu Ser Arg Lys Lys Thr Lys Gln Thr Met Ile Ser Glu Leu Asp Glu
        450                 455                 460

ttc gaa gat gaa gac agt gat ttg tac ata gag aac gac cca atc gtc     1440
Phe Glu Asp Glu Asp Ser Asp Leu Tyr Ile Glu Asn Asp Pro Ile Val
465                 470                 475                 480

caa gcc att gag aat gag aat aaa aga caa tga                         1473
Gln Ala Ile Glu Asn Glu Asn Lys Arg Gln
                485                 490
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<210>   54

<211>   490

<212>   PRT

<213>   Arabidopsis thaliana

<400>   54

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Met Gln Thr Phe Ser Ile Ser Leu Leu Arg His Ser Ser Pro Phe Leu
1               5                   10                  15


Arg His Thr Ala Ile Phe His Gly Gly Val Gly Val Arg Phe Lys Phe
        20                  25                  30


Leu Arg Ser Phe Ser Pro Leu Ser Ala Arg Arg Asp Asn Pro Asp Val
        35                  40                  45
```

Ser Arg Lys Pro Gln Pro Ser Lys Asn Met Leu Arg Ala Lys His Ile
    50   55   60

Gly Lys Asn Tyr Ser Ser Ser Leu Ser Pro Val Leu Ser Pro Glu His
65   70   75   80

Lys Pro Ser Leu Leu Glu Ser Gln Ala Ile Gly Thr Val Ala Thr Ala
            85   90   95

Gln Ala Asn Phe Met Arg Val Ile Val Gln Asp Val Ala Asn Ser Val
            100   105   110

Thr Ser Asp Asp Asp Asn Asp Ser Ser Lys Thr Gly Val Glu Leu Leu
        115   120   125

Cys Val Val Arg Ala Val Leu Lys Lys Ile Arg Arg Arg Val Leu Val
    130   135   ·140

Gly Asp Lys Val Leu Val Gly Ser Ile Asp Trp Val Asp Arg Arg Gly
145   150   155   160

Met Ile Glu Asn Val Phe His Arg Arg Ser Glu Ile Leu Asp Pro Pro
                165   170   175

Val Ala Asn Val Asp His Leu Leu Val Leu Phe Ser Leu Asp Gln Pro
            180   185   190

Lys Leu Glu Pro Phe Thr Leu Thr Arg Phe Leu Val Glu Ala Glu Ser
        195   200   205

Thr Arg Ile Pro Leu Thr Leu Ala Leu Asn Lys Thr Glu Leu Ile Ser
    210   215   220

Glu Glu Glu Leu Glu Thr Trp Lys Ile Arg Leu Arg Gly Trp Asn Tyr
225   230   235   240

Glu Pro Leu Phe Cys Ser Val Gly Thr Lys Asp Gly Leu Asp Asp Ile
            245   250   255

Ala Phe Val Leu Arg Asp Gln Thr Ser Val Ile Val Gly Pro Ser Gly
            260   265   270

Val Gly Lys Ser Ser Leu Ile Asn Val Leu Arg Ser Asn His Gly Gly
    275   280   285

126

```
Gly Val Val Glu Asp Glu Asn Trp Phe Glu Pro Met Leu Gly Asn Lys
     290                 295                 300

Trp Phe Asp Asp Gln Arg Val Gly Glu Val Ser Ser Arg Ser Gly Arg
3.5               310                 315                 320

Gly Lys His Thr Thr Arg Asn Val Ser Leu Leu Pro Val Ser Glu Gly
              325                 330                 335

Gly Tyr Leu Ala Asp Thr Pro Gly Phe Asn Gln Pro Ser Leu Leu Lys
              340                 345                 350

Val Thr Lys His Ser Leu Ala His Cys Phe Pro Glu Ile Arg Asn Met
         355                 360                 365

Ile Glu Ser Glu Lys Cys Gly Phe Arg Asp Cys Leu His Ile Gly Glu
     370                 375                 380

Pro Gly Cys Val Val Lys Gly Asp Trp Glu Arg Tyr Pro Tyr Tyr Leu
385                 390                 395                 400

Gln Leu Leu Asp Glu Ile Arg Ile Arg Glu Glu Phe Gln Leu Arg Thr
              405                 410                 415

Phe Gly Thr Lys Arg Glu Asp Asp Val Arg Tyr Lys Val Gly Asp Met
              420                 425                 430

Gly Val Lys His Ala Glu Pro Arg Leu Met Pro Lys Lys His Arg Arg
              435                 440                 445

Glu Ser Arg Lys Lys Thr Lys Gln Thr Met Ile Ser Glu Leu Asp Glu
     450                 455                 460

Phe Glu Asp Glu Asp Ser Asp Leu Tyr Ile Glu Asn Asp Pro Ile Val
465                 470                 475                 480

Gln Ala Ile Glu Asn Glu Asn Lys Arg Gln
              485                 490
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<210>  55

<211>  897
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<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(897)

<223> 35154

<400> 55
atg gtg ttt gga caa gta gta ata ggt cct cca gga tcg gga aag acc   48
Met Val Phe Gly Gln Val Val Ile Gly Pro Pro Gly Ser Gly Lys Thr
1   5   10   15

act tat tgc aat gga atg tct cag ttc ctc tct cta atg ggc agg aag   96
Thr Tyr Cys Asn Gly Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys
            20   25   30

gtt gct att gtt aat ctg gat cct gca aat gat gca tta cct tat gag   144
Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu
        35   40   45

tgt ggt gtg aat ata gaa gaa ttg atc aag tta gaa gat gtt atg tcg   192
Cys Gly Val Asn Ile Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser
    50   55   60

gaa cac tcg ctt ggt cct aat gga ggt ctt gta tat tgt atg gag tac   240
Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr
65   70   75   80

ttg gag aaa aac att gac tgg ctg gaa tct aaa cta aag cct ctt ctg   288
Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu
                85   90   95

aag gat cat tac att ctc ttt gat ttt cct ggc caa gtg gaa ttg ttc   336
Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe
            100   105   110

ttc att cat gac agt acc aag aat gtt ctc acg aag ctg att aaa tca   384
Phe Ile His Asp Ser Thr Lys Asn Val Leu Thr Lys Leu Ile Lys Ser
            115   120   125

ttg aac ctt aga tta act gct gtg caa cta att gat tcc cat cta tgt   432
Leu Asn Leu Arg Leu Thr Ala Val Gln Leu Ile Asp Ser His Leu Cys
        130   135   140

tgt gat ccc ggg aac tac gta agt tcg cta ctt ctc tcc tta tcc aca   480
Cys Asp Pro Gly Asn Tyr Val Ser Ser Leu Leu Leu Ser Leu Ser Thr
145   150   155   160

atg ctt cac atg gaa ctc cca cat gtc aat gta ttg tct aaa atc gat   528
Met Leu His Met Glu Leu Pro His Val Asn Val Leu Ser Lys Ile Asp
                165   170   175

128

```
ctg att gga agc tac ggg aag cta gct ttc aat tta gat ttc tat acc      576
Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr
            180             185             190

gat gtt caa gac ttg tca tac ttg gag cac cat ctt agt caa gat cct      624
Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro
        195             200             205

cgc tct gct aag tac aga aaa cta aca aaa gag cta tgt agt gtc att      672
Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile
        210             215             220

gaa gat tac agt ctt gtt aat ttt aca acc ttg gat att cag gat aaa      720
Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys
225             230             235             240

gaa agt gtt ggg gat cta gta aag ctc atc gac aag agc aat gga tac      768
Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr
            245             250             255

ata ttt gcc ggc att gat gca agt gtg gtt gaa tac agc aag att gca      816
Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala
            260             265             270

att ggt caa act gat tgg gat tat aac aga gtc gca gct gta cag gag      864
Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu
            275             280             285

aag tac atg gaa gat gag gaa ata caa gac tga                          897
Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp
            290             295
```

<210> 56

<211> 298

<212> PRT

<213> Arabidopsis thaliana

<400> 56

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Met Val Phe Gly Gln Val Val Ile Gly Pro Pro Gly Ser Gly Lys Thr
1               5               10              15


Thr Tyr Cys Asn Gly Met Ser Gln Phe Leu Ser Leu Met Gly Arg Lys
            20              25              30


Val Ala Ile Val Asn Leu Asp Pro Ala Asn Asp Ala Leu Pro Tyr Glu
            35              40              45


Cys Gly Val Asn Ile Glu Glu Leu Ile Lys Leu Glu Asp Val Met Ser
            50              55              60
```

Glu His Ser Leu Gly Pro Asn Gly Gly Leu Val Tyr Cys Met Glu Tyr
65   70   75   80

Leu Glu Lys Asn Ile Asp Trp Leu Glu Ser Lys Leu Lys Pro Leu Leu
                85   90   95

Lys Asp His Tyr Ile Leu Phe Asp Phe Pro Gly Gln Val Glu Leu Phe
            100   105   110

Phe Ile His Asp Ser Thr Lys Asn Val Leu Thr Lys Leu Ile Lys Ser
        115   120   125

Leu Asn Leu Arg Leu Thr Ala Val Gln Leu Ile Asp Ser His Leu Cys
    130   135   140

Cys Asp Pro Gly Asn Tyr Val Ser Ser Leu Leu Leu Ser Leu Ser Thr
145   150   155   160

Met Leu His Met Glu Leu Pro His Val Asn Val Leu Ser Lys Ile Asp
            165   170   175

Leu Ile Gly Ser Tyr Gly Lys Leu Ala Phe Asn Leu Asp Phe Tyr Thr
        180   185   190

Asp Val Gln Asp Leu Ser Tyr Leu Glu His His Leu Ser Gln Asp Pro
    195   200   205

Arg Ser Ala Lys Tyr Arg Lys Leu Thr Lys Glu Leu Cys Ser Val Ile
    210   215   220

Glu Asp Tyr Ser Leu Val Asn Phe Thr Thr Leu Asp Ile Gln Asp Lys
225   230   235   240

Glu Ser Val Gly Asp Leu Val Lys Leu Ile Asp Lys Ser Asn Gly Tyr
            245   250   255

Ile Phe Ala Gly Ile Asp Ala Ser Val Val Glu Tyr Ser Lys Ile Ala
            260   265   270

Ile Gly Gln Thr Asp Trp Asp Tyr Asn Arg Val Ala Ala Val Gln Glu
    275   280   285

Lys Tyr Met Glu Asp Glu Glu Ile Gln Asp
    290   295

130

<210> 57

<211> 849

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(849)

<223> 35438

<400> 57
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atg gaa gct ctc tac gcc aag ctc tac gac aaa tac acc aaa ctc cag      48
Met Glu Ala Leu Tyr Ala Lys Leu Tyr Asp Lys Tyr Thr Lys Leu Gln
1               5                  10                  15

aag aag aaa tat tcc gaa tac gat gag att aat aag gaa caa gaa gag      96
Lys Lys Lys Tyr Ser Glu Tyr Asp Glu Ile Asn Lys Glu Gln Glu Glu
            20                  25                  30

aaa ttc ctt acc ttt gtt tca gcc tca gag gag ttg atg gaa cat ttg     144
Lys Phe Leu Thr Phe Val Ser Ala Ser Glu Glu Leu Met Glu His Leu
        35                  40                  45

aga ggt gaa aat cag agt tct ctg gag atg gtt gag aag ttg agg aat     192
Arg Gly Glu Asn Gln Ser Ser Leu Glu Met Val Glu Lys Leu Arg Asn
    50                  55                  60

gaa atc att tca atc aga tct ggc agg gac gac aag ttt ctg gag tgt     240
Glu Ile Ile Ser Ile Arg Ser Gly Arg Asp Asp Lys Phe Leu Glu Cys
65                  70                  75                  80

caa aag ctt ctc atg gaa gaa gaa cta aag aac aaa tca ctt tct gaa     288
Gln Lys Leu Leu Met Glu Glu Glu Leu Lys Asn Lys Ser Leu Ser Glu
                85                  90                  95

gaa gtt gtc aag cta aaa gag ctg gtc caa gag gaa cat cct cgc aac     336
Glu Val Val Lys Leu Lys Glu Leu Val Gln Glu Glu His Pro Arg Asn
            100                 105                 110

tat gaa gat caa agt gga aaa aaa caa aag aga aag act cct gaa agt     384
Tyr Glu Asp Gln Ser Gly Lys Lys Gln Lys Arg Lys Thr Pro Glu Ser
        115                 120                 125

gct cga gtt aca acg aga agc atg ata aaa cgt agc aga ctg tca gaa     432
Ala Arg Val Thr Thr Arg Ser Met Ile Lys Arg Ser Arg Leu Ser Glu
    130                 135                 140

gat ttg gtg gaa acg gat atg gta tca cct gac att agc aaa cat cat     480
```

131

```
Asp Leu Val Glu Thr Asp Met Val Ser Pro Asp Ile Ser Lys His His
145                 150                 155                 160

aaa gca aag gag cct ctc ttg gtt tct cag cca caa tgc tgc aga aca      528
Lys Ala Lys Glu Pro Leu Leu Val Ser Gln Pro Gln Cys Cys Arg Thr
                    165             170                 175

acc tac gat gga tca agt agt tct gct agt tgt aca ttt caa gct ctt      576
Thr Tyr Asp Gly Ser Ser Ser Ser Ala Ser Cys Thr Phe Gln Ala Leu
                180             185                 190

ggc aaa cac ttg cta gga atg aaa tta tca act aat aat aag ggc aaa      624
Gly Lys His Leu Leu Gly Met Lys Leu Ser Thr Asn Asn Lys Gly Lys
            195                 200                 205

cgc gcc tgc att gta gcc tca cac cca aca acc ggt tta tcc ttc agc      672
Arg Ala Cys Ile Val Ala Ser His Pro Thr Thr Gly Leu Ser Phe Ser
        210                 215                 220

cta act ttt ata aat aac cca aat ggt gaa gaa tct gag ctg ctt tac      720
Leu Thr Phe Ile Asn Asn Pro Asn Gly Glu Glu Ser Glu Leu Leu Tyr
225                 230                 235                 240

aag cct gca tca ctc gga aca ttt caa aga gtg gca ccg gaa tgg atg      768
Lys Pro Ala Ser Leu Gly Thr Phe Gln Arg Val Ala Pro Glu Trp Met
                    245             250                 255

aga gaa gtt ata aag ttc agc aca agt atg tgt ccc atc ttc ttt gaa      816
Arg Glu Val Ile Lys Phe Ser Thr Ser Met Cys Pro Ile Phe Phe Glu
                260             265                 270

aga gtc tct cga gtc att aag ctc aat tgt tga                          849
Arg Val Ser Arg Val Ile Lys Leu Asn Cys
            275                 280
```

```
<210>   58

<211>   282

<212>   PRT

<213>   Arabidopsis thaliana



<400>   58

Met Glu Ala Leu Tyr Ala Lys Leu Tyr Asp Lys Tyr Thr Lys Leu Gln
1               5                   10                  15


Lys Lys Lys Tyr Ser Glu Tyr Asp Glu Ile Asn Lys Glu Gln Glu Glu
            20                  25                  30


Lys Phe Leu Thr Phe Val Ser Ala Ser Glu Glu Leu Met Glu His Leu
        35                  40                  45
```

132

```
Arg Gly Glu Asn Gln Ser Ser Leu Glu Met Val Glu Lys Leu Arg Asn
    50                  55                  60

Glu Ile Ile Ser Ile Arg Ser Gly Arg Asp Asp Lys Phe Leu Glu Cys
65                  70                  75                  80

Gln Lys Leu Leu Met Glu Glu Glu Leu Lys Asn Lys Ser Leu Ser Glu
                85                  90                  95

Glu Val Val Lys Leu Lys Glu Leu Val Gln Glu Glu His Pro Arg Asn
                100                 105                 110

Tyr Glu Asp Gln Ser Gly Lys Lys Gln Lys Arg Lys Thr Pro Glu Ser
        115                 120                 125

Ala Arg Val Thr Thr Arg Ser Met Ile Lys Arg Ser Arg Leu Ser Glu
    130                 135                 140

Asp Leu Val Glu Thr Asp Met Val Ser Pro Asp Ile Ser Lys His His
145                 150                 155                 160

Lys Ala Lys Glu Pro Leu Leu Val Ser Gln Pro Gln Cys Cys Arg Thr
                165                 170                 175

Thr Tyr Asp Gly Ser Ser Ser Ser Ala Ser Cys Thr Phe Gln Ala Leu
            180                 185                 190

Gly Lys His Leu Leu Gly Met Lys Leu Ser Thr Asn Asn Lys Gly Lys
        195                 200                 205

Arg Ala Cys Ile Val Ala Ser His Pro Thr Thr Gly Leu Ser Phe Ser
    210                 215                 220

Leu Thr Phe Ile Asn Asn Pro Asn Gly Glu Glu Ser Glu Leu Leu Tyr
225                 230                 235                 240

Lys Pro Ala Ser Leu Gly Thr Phe Gln Arg Val Ala Pro Glu Trp Met
                245                 250                 255

Arg Glu Val Ile Lys Phe Ser Thr Ser Met Cys Pro Ile Phe Phe Glu
                260                 265                 270

Arg Val Ser Arg Val Ile Lys Leu Asn Cys
    275                 280
```

133

<210> 59

<211> 1467

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1467)

<223> 37351

<400> 59

atg	gaa	ttg	gat	tcg	gag	aac	aaa	ttg	ttg	aag	acg	ggt	ttg	gtt	ata		48
Met	Glu	Leu	Asp	Ser	Glu	Asn	Lys	Leu	Leu	Lys	Thr	Gly	Leu	Val	Ile		
1				5					10					15			

gtg	gcg	aca	ctt	gtt	ata	gcc	aaa	ctc	atc	ttc	tct	ttc	ttc	act	tct	96
Val	Ala	Thr	Leu	Val	Ile	Ala	Lys	Leu	Ile	Phe	Ser	Phe	Phe	Thr	Ser	
		20					25					30				

gat	tct	aag	aag	aag	cgt	ctt	cct	cct	act	ctt	aaa	gct	tgg	cct	cca	144
Asp	Ser	Lys	Lys	Lys	Arg	Leu	Pro	Pro	Thr	Leu	Lys	Ala	Trp	Pro	Pro	
		35					40					45				

ttg	gtt	gga	agt	ctt	atc	aaa	ttc	ttg	aaa	gga	cct	att	att	atg	ctt	192
Leu	Val	Gly	Ser	Leu	Ile	Lys	Phe	Leu	Lys	Gly	Pro	Ile	Ile	Met	Leu	
	50					55					60					

aga	gag	gaa	tac	cct	aag	ctt	gga	agt	gtg	ttt	act	gtt	aat	ctt	gtt	240
Arg	Glu	Glu	Tyr	Pro	Lys	Leu	Gly	Ser	Val	Phe	Thr	Val	Asn	Leu	Val	
65					70				75						80	

cac	aaa	aag	att	act	ttt	ctt	att	ggt	cct	gaa	gtc	tct	gct	cat	ttt	288
His	Lys	Lys	Ile	Thr	Phe	Leu	Ile	Gly	Pro	Glu	Val	Ser	Ala	His	Phe	
				85					90					95		

ttc	aaa	gct	tct	gaa	tct	gat	ctt	agt	cag	cag	gaa	gtg	tat	cag	ttc	336
Phe	Lys	Ala	Ser	Glu	Ser	Asp	Leu	Ser	Gln	Gln	Glu	Val	Tyr	Gln	Phe	
			100					105					110			

aat	gtc	cct	act	ttt	ggt	cct	gga	gtt	gtt	ttc	gat	gtt	gat	tat	tct	384
Asn	Val	Pro	Thr	Phe	Gly	Pro	Gly	Val	Val	Phe	Asp	Val	Asp	Tyr	Ser	
		115					120					125				

gtt	cgt	cag	gag	cag	ttt	cgg	ttc	ttc	act	gag	gca	ctt	aga	gtt	aac	432
Val	Arg	Gln	Glu	Gln	Phe	Arg	Phe	Phe	Thr	Glu	Ala	Leu	Arg	Val	Asn	
	130					135					140					

aag	ttg	aag	ggt	tat	gtg	gat	atg	atg	gtt	act	gaa	gct	gag	gat	tac	480
Lys	Leu	Lys	Gly	Tyr	Val	Asp	Met	Met	Val	Thr	Glu	Ala	Glu	Asp	Tyr	
145				150					155					160		

134

ttc tct aaa tgg gga gag agt ggt gaa gtt gat att aag gtt gag cta   528
Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu
                165   170   175

gag agg ctc atc atc ttg act gca agt aga tgt tta ctg ggt cga gaa   576
Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu
                180   185   190

gtt cgt gat cag ctt ttt gat gat gtc tct gct ttg ttc cat gac ctt   624
Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu
                195   200   205

gac aat gga atg ctt ccc atc agt gtt ctc ttc cca tat ctc cca att   672
Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile
        210   215   220

cca gct cac cgc cgt cgt gac cgt gcc cga gaa aag ctt tcg gag att   720
Pro Ala His Arg Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile
225   230   235   240

ttc gca aaa atc att ggg tcg aga aaa cgc tct gga aaa aca gag aac   768
Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn
                245   250   255

gac atg ctg cag tgt ttc atc gaa tca aag tac aaa gat ggt aga cag   816
Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln
                260   265   270

aca acc gaa tct gaa gtc act ggt ttg ctc att gct gct ctg ttt gca   864
Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala
                275   280   285

gga caa cac acg agc tct atc act tcc acc tgg acc ggt gct tat ctg   912
Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu
        290   295   300

atg cga tac aaa gag tac ttc tca gct gct ctt gat gag cag aag aac   960
Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn
305   310   315   320

ctg att gcg aaa cat gga gac aag atc gat cat gat atc tta tcc gag   1008
Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu
                325   330   335

atg gat gtt ctc tac cgc tgc att aag gaa gcg ttg agg ctt cac cct   1056
Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro
                340   345   350

cca ctc atc atg tta atg aga gcc tcg cac agt gat ttc agc gtg aca   1104
Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr
                355   360   365

gct cgg gat gga aaa act tac gat atc cca aag ggt cac atc gtt gca   1152
Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala
        370   375   380

acc tcc cct gca ttt gcc aac cgc tta ccg cac atc ttc aaa gac ccc   1200
Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro
385   390   395   400

135

```
gac acc tac gac cca gaa aga ttc tcc cct gga aga gaa gag gac aaa        1248
Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys
            405                 410                 415

gcc gca ggg gca ttc tcg tac att gca ttc gga ggg gga agg cac ggg        1296
Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Gly Arg His Gly
            420                 425                 430

tgc ctt gga gag ccg ttt gct tac ctg cag atc aaa gcc ata tgg agt        1344
Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser
            435                 440                 445

cat ttg ttg agg aac ttc gag ctt gag cta gtt tca ccg ttc cct gag        1392
His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu
        450                 455                 460

att gac tgg aac gct atg gtg gtt gga gtt aaa ggc aat gtg atg gtg        1440
Ile Asp Trp Asn Ala Met Val Val Gly Val Lys Gly Asn Val Met Val
465                 470                 475                 480

cgt tac aag agg cgc cag ctt tct taa                                    1467
Arg Tyr Lys Arg Arg Gln Leu Ser
                485
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<210> 60

<211> 488

<212> PRT

<213> Arabidopsis thaliana

<400> 60

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Met Glu Leu Asp Ser Glu Asn Lys Leu Leu Lys Thr Gly Leu Val Ile
1               5               10              15

Val Ala Thr Leu Val Ile Ala Lys Leu Ile Phe Ser Phe Phe Thr Ser
            20              25              30

Asp Ser Lys Lys Lys Arg Leu Pro Pro Thr Leu Lys Ala Trp Pro Pro
            35              40              45

Leu Val Gly Ser Leu Ile Lys Phe Leu Lys Gly Pro Ile Ile Met Leu
        50              55              60

Arg Glu Glu Tyr Pro Lys Leu Gly Ser Val Phe Thr Val Asn Leu Val
65              70              75              80

His Lys Lys Ile Thr Phe Leu Ile Gly Pro Glu Val Ser Ala His Phe
                85              90              95
```

Phe Lys Ala Ser Glu Ser Asp Leu Ser Gln Gln Glu Val Tyr Gln Phe
        100   105   110

Asn Val Pro Thr Phe Gly Pro Gly Val Val Phe Asp Val Asp Tyr Ser
        115   120   125

Val Arg Gln Glu Gln Phe Arg Phe Phe Thr Glu Ala Leu Arg Val Asn
        130   135   140

Lys Leu Lys Gly Tyr Val Asp Met Met Val Thr Glu Ala Glu Asp Tyr
145   150   155   160

Phe Ser Lys Trp Gly Glu Ser Gly Glu Val Asp Ile Lys Val Glu Leu
                165   170   175

Glu Arg Leu Ile Ile Leu Thr Ala Ser Arg Cys Leu Leu Gly Arg Glu
            180   185   190

Val Arg Asp Gln Leu Phe Asp Asp Val Ser Ala Leu Phe His Asp Leu
        195   200   205

Asp Asn Gly Met Leu Pro Ile Ser Val Leu Phe Pro Tyr Leu Pro Ile
        210   215   220

Pro Ala His Arg Arg Arg Asp Arg Ala Arg Glu Lys Leu Ser Glu Ile
225   230   235   240

Phe Ala Lys Ile Ile Gly Ser Arg Lys Arg Ser Gly Lys Thr Glu Asn
                245   250   255

Asp Met Leu Gln Cys Phe Ile Glu Ser Lys Tyr Lys Asp Gly Arg Gln
            260   265   270

Thr Thr Glu Ser Glu Val Thr Gly Leu Leu Ile Ala Ala Leu Phe Ala
        275   280   285

Gly Gln His Thr Ser Ser Ile Thr Ser Thr Trp Thr Gly Ala Tyr Leu
        290   295   300

Met Arg Tyr Lys Glu Tyr Phe Ser Ala Ala Leu Asp Glu Gln Lys Asn
305   310   315   320

Leu Ile Ala Lys His Gly Asp Lys Ile Asp His Asp Ile Leu Ser Glu
                325   330   335

137

Met Asp Val Leu Tyr Arg Cys Ile Lys Glu Ala Leu Arg Leu His Pro
              340   345   350

Pro Leu Ile Met Leu Met Arg Ala Ser His Ser Asp Phe Ser Val Thr
              355   360   365

Ala Arg Asp Gly Lys Thr Tyr Asp Ile Pro Lys Gly His Ile Val Ala
              370   375   380

Thr Ser Pro Ala Phe Ala Asn Arg Leu Pro His Ile Phe Lys Asp Pro
385   390   395   400

Asp Thr Tyr Asp Pro Glu Arg Phe Ser Pro Gly Arg Glu Glu Asp Lys
                   405   410   415

Ala Ala Gly Ala Phe Ser Tyr Ile Ala Phe Gly Gly Gly Arg His Gly
              420   425   430

Cys Leu Gly Glu Pro Phe Ala Tyr Leu Gln Ile Lys Ala Ile Trp Ser
              435   440   445

His Leu Leu Arg Asn Phe Glu Leu Glu Leu Val Ser Pro Phe Pro Glu
    450   455   460

Ile Asp Trp Asn Ala Met Val Val Gly Val Lys Gly Asn Val Met Val
465   470   475   480

Arg Tyr Lys Arg Arg Gln Leu Ser
                   485

<210> 61

<211> 1836

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1836)

<223> 37389

138

<400> 61

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atg ggg att gtt ttg gaa cct cct tgt cct aaa agt gtt gat ggg att        48
Met Gly Ile Val Leu Glu Pro Pro Cys Pro Lys Ser Val Asp Gly Ile
1               5                   10                  15

agc att gat cct gag cct aat tgg aat ttc gag agt ttg gtc gct gag        96
Ser Ile Asp Pro Glu Pro Asn Trp Asn Phe Glu Ser Leu Val Ala Glu
            20                  25                  30

att gct tct gtt gaa aag aag ctc aat ggc ttc tca atg tat cct cag       144
Ile Ala Ser Val Glu Lys Lys Leu Asn Gly Phe Ser Met Tyr Pro Gln
        35                  40                  45

cca att act aac aca acc tta cgg atg gga agg aga ggt gga gga ttt       192
Pro Ile Thr Asn Thr Thr Leu Arg Met Gly Arg Arg Gly Gly Gly Phe
    50                  55                  60

gta atg cat gtc tca gaa gat gag atg gag agt gac gaa ggt gaa gag       240
Val Met His Val Ser Glu Asp Glu Met Glu Ser Asp Glu Gly Glu Glu
65                  70                  75                  80

agt gat gat gag gaa gaa gaa gaa gat cat agt caa atc tgt aca gcg       288
Ser Asp Asp Glu Glu Glu Glu Glu Asp His Ser Gln Ile Cys Thr Ala
                85                  90                  95

gga aaa cgt ttt gcc tgt gat gag ctt tac ttg agt gat gaa tct gat       336
Gly Lys Arg Phe Ala Cys Asp Glu Leu Tyr Leu Ser Asp Glu Ser Asp
            100                 105                 110

gaa gag ttt gat cat gaa cct gag tat atg atg aat aag ttg ggt ctg       384
Glu Glu Phe Asp His Glu Pro Glu Tyr Met Met Asn Lys Leu Gly Leu
        115                 120                 125

gct gag agt gcc cta tat gag gtt atc aac gac cac caa acc gaa atc       432
Ala Glu Ser Ala Leu Tyr Glu Val Ile Asn Asp His Gln Thr Glu Ile
    130                 135                 140

aag gac gac att agg aat caa gta tca gtt gtt gaa aca gaa ata atg       480
Lys Asp Asp Ile Arg Asn Gln Val Ser Val Val Glu Thr Glu Ile Met
145                 150                 155                 160

aat gag att gaa acg tct ctc tct gcc ata gcc cgg gtt gaa aag tac       528
Asn Glu Ile Glu Thr Ser Leu Ser Ala Ile Ala Arg Val Glu Lys Tyr
                165                 170                 175

agt gag act cgg aaa gaa gtt gaa cgg aaa ctt gat ctt caa tat cag       576
Ser Glu Thr Arg Lys Glu Val Glu Arg Lys Leu Asp Leu Gln Tyr Gln
            180                 185                 190

cga aaa gtt gct gaa gca ctt gat acc cat ctg act gca gtc caa cgc       624
Arg Lys Val Ala Glu Ala Leu Asp Thr His Leu Thr Ala Val Gln Arg
        195                 200                 205

gaa cat aaa att aaa tcg caa ata gaa gaa aga aag ata agg agc gag       672
Glu His Lys Ile Lys Ser Gln Ile Glu Glu Arg Lys Ile Arg Ser Glu
    210                 215                 220

gaa gct cag gag gag gcc agg agg aag gaa agg gct cat caa gaa gag       720
```

139

```
Glu Ala Gln Glu Glu Ala Arg Arg Lys Glu Arg Ala His Gln Glu Glu
225               230             235               240
```

```
aaa ata cgt caa gaa aaa gct cgc gca gag gct caa atg cta gca aaa    768
Lys Ile Arg Gln Glu Lys Ala Arg Ala Glu Ala Gln Met Leu Ala Lys
                245             250             255
```

```
atc aga gct gaa gaa gaa aag aaa gaa gtt gag aga aag gca gcc aga    816
Ile Arg Ala Glu Glu Glu Lys Lys Glu Val Glu Arg Lys Ala Ala Arg
                260             265             270
```

```
gaa gta gct gaa aaa gaa gta gca gat cgc aaa gct gcc gaa caa aaa    864
Glu Val Ala Glu Lys Glu Val Ala Asp Arg Lys Ala Ala Glu Gln Lys
                275             280             285
```

```
ctt gcg gaa cag aag gct gtg ata gag agt gtt acg ggg agt tca gct    912
Leu Ala Glu Gln Lys Ala Val Ile Glu Ser Val Thr Gly Ser Ser Ala
                290             295             300
```

```
aca tca aat gct caa gct ggg ggt aat tca atc cga gct gca gaa agt    960
Thr Ser Asn Ala Gln Ala Gly Gly Asn Ser Ile Arg Ala Ala Glu Ser
305             310             315             320
```

```
gct ttg ata ttg gag aac cac aga ttg aaa aag ctc gaa gaa cta gaa    1008
Ala Leu Ile Leu Glu Asn His Arg Leu Lys Lys Leu Glu Glu Leu Glu
                325             330             335
```

```
aca acg aac caa tcg ctt aag tca cgt tca aat gaa aac ttt agc agt    1056
Thr Thr Asn Gln Ser Leu Lys Ser Arg Ser Asn Glu Asn Phe Ser Ser
                340             345             350
```

```
ttt gag aag cat att gga aga gtg ata agg caa ata agt ggg aca aag    1104
Phe Glu Lys His Ile Gly Arg Val Ile Arg Gln Ile Ser Gly Thr Lys
                355             360             365
```

```
gat agt gta agt ggg aaa atc aat gat att gtg aaa ata ttt aaa gac    1152
Asp Ser Val Ser Gly Lys Ile Asn Asp Ile Val Lys Ile Phe Lys Asp
370             375             380
```

```
cct cgt tgt ccg gta tcc ata agt att gca gct ttt gca aag aag atg    1200
Pro Arg Cys Pro Val Ser Ile Ser Ile Ala Ala Phe Ala Lys Lys Met
385             390             395             400
```

```
gtc acc act aag gaa aaa cca aac cct ttt gca tgc agc tat gtc att    1248
Val Thr Thr Lys Glu Lys Pro Asn Pro Phe Ala Cys Ser Tyr Val Ile
                405             410             415
```

```
gtt tac atc aac tca cag ttt ccc caa gtt atg gat att ctt ctc gcg    1296
Val Tyr Ile Asn Ser Gln Phe Pro Gln Val Met Asp Ile Leu Leu Ala
                420             425             430
```

```
gaa ttc cac aaa gct tgc att tac act gtc cca aag cat att gta aac    1344
Glu Phe His Lys Ala Cys Ile Tyr Thr Val Pro Lys His Ile Val Asn
                435             440             445
```

```
tca cag tca gct tgg gat tca gac gca tat gaa cgc cta gat tct ata    1392
Ser Gln Ser Ala Trp Asp Ser Asp Ala Tyr Glu Arg Leu Asp Ser Ile
                450             455             460
```

```
atg agg ctc tac ggt gca ctt gtt cag acc gat atc cgc gtt ggc aat    1440
```

140

```
Met Arg Leu Tyr Gly Ala Leu Val Gln Thr Asp Ile Arg Val Gly Asn
465                 470             475             480

gct act aac gtt cat ggg ata gaa cat gga tgg gct tgg tta gcc cgg    1488
Ala Thr Asn Val His Gly Ile Glu His Gly Trp Ala Trp Leu Ala Arg
                485             490             495

ttc ctt aac aaa atc cca gcc aac aga gcc act gcg aca gcc ttg aac    1536
Phe Leu Asn Lys Ile Pro Ala Asn Arg Ala Thr Ala Thr Ala Leu Asn
                500             505             510

tcc ttt ctc cag acg gct ggg ttt ggt ctt cat cag agg tac aaa tct    1584
Ser Phe Leu Gln Thr Ala Gly Phe Gly Leu His Gln Arg Tyr Lys Ser
                515             520             525

cag ttt ctg aag gtt gtg aat gtt gtg aga gag cat ttc ttg cag aaa    1632
Gln Phe Leu Lys Val Val Asn Val Val Arg Glu His Phe Leu Gln Lys
        530             535             540

ttg cgg gcg aag aag gac acg tcg gat cta ctt gtg atc ata gcc gaa    1680
Leu Arg Ala Lys Lys Asp Thr Ser Asp Leu Leu Val Ile Ile Ala Glu
545             550             555             560

atc aca gcg tac tta gat gac cgg atg tat ctc aag gaa cct gaa gga    1728
Ile Thr Ala Tyr Leu Asp Asp Arg Met Tyr Leu Lys Glu Pro Glu Gly
                565             570             575

aga gct atg aag acg act agt acc ttg tcc tct gaa ctt act gct gaa    1776
Arg Ala Met Lys Thr Thr Ser Thr Leu Ser Ser Glu Leu Thr Ala Glu
                580             585             590

tta aat cag ccg aac tac aat cag aat tac cag agg aat gat tac aga    1824
Leu Asn Gln Pro Asn Tyr Asn Gln Asn Tyr Gln Arg Asn Asp Tyr Arg
                595             600             605

aac tac tat tga                                                    1836
Asn Tyr Tyr
        610


<210>   62

<211>   611

<212>   PRT

<213>   Arabidopsis thaliana



<400>   62

Met Gly Ile Val Leu Glu Pro Pro Cys Pro Lys Ser Val Asp Gly Ile
1               5               10              15


Ser Ile Asp Pro Glu Pro Asn Trp Asn Phe Glu Ser Leu Val Ala Glu
            20              25              30
```

141

Ile Ala Ser Val Glu Lys Lys Leu Asn Gly Phe Ser Met Tyr Pro Gln
        35   40   45

Pro Ile Thr Asn Thr Thr Leu Arg Met Gly Arg Arg Gly Gly Gly Phe
        50   55   60

Val Met His Val Ser Glu Asp Glu Met Glu Ser Asp Glu Gly Glu Glu
65   70   75   80

Ser Asp Asp Glu Glu Glu Glu Glu Asp His Ser Gln Ile Cys Thr Ala
                85   90   95

Gly Lys Arg Phe Ala Cys Asp Glu Leu Tyr Leu Ser Asp Glu Ser Asp
            100   105   110

Glu Glu Phe Asp His Glu Pro Glu Tyr Met Met Asn Lys Leu Gly Leu
            115   120   125

Ala Glu Ser Ala Leu Tyr Glu Val Ile Asn Asp His Gln Thr Glu Ile
        130   135   140

Lys Asp Asp Ile Arg Asn Gln Val Ser Val Val Glu Thr Glu Ile Met
145   150   155   160

Asn Glu Ile Glu Thr Ser Leu Ser Ala Ile Ala Arg Val Glu Lys Tyr
                165   170   175

Ser Glu Thr Arg Lys Glu Val Glu Arg Lys Leu Asp Leu Gln Tyr Gln
            180   185   190

Arg Lys Val Ala Glu Ala Leu Asp Thr His Leu Thr Ala Val Gln Arg
        195   200   205

Glu His Lys Ile Lys Ser Gln Ile Glu Glu Arg Lys Ile Arg Ser Glu
        210   215   220

Glu Ala Gln Glu Glu Ala Arg Arg Lys Glu Arg Ala His Gln Glu Glu
225   230   235   240

Lys Ile Arg Gln Glu Lys Ala Arg Ala Glu Ala Gln Met Leu Ala Lys
            245   250   255

Ile Arg Ala Glu Glu Glu Lys Lys Glu Val Glu Arg Lys Ala Ala Arg
            260   265   270

Glu Val Ala Glu Lys Glu Val Ala Asp Arg Lys Ala Ala Glu Gln Lys
         275   280   285

Leu Ala Glu Gln Lys Ala Val Ile Glu Ser Val Thr Gly Ser Ser Ala
         290   295   300

Thr Ser Asn Ala Gln Ala Gly Gly Asn Ser Ile Arg Ala Ala Glu Ser
305   310   315   320

Ala Leu Ile Leu Glu Asn His Arg Leu Lys Lys Leu Glu Glu Leu Glu
                 325   330   335

Thr Thr Asn Gln Ser Leu Lys Ser Arg Ser Asn Glu Asn Phe Ser Ser
                 340   345   350

Phe Glu Lys His Ile Gly Arg Val Ile Arg Gln Ile Ser Gly Thr Lys
         355   360   365

Asp Ser Val Ser Gly Lys Ile Asn Asp Ile Val Lys Ile Phe Lys Asp
         370   375   380

Pro Arg Cys Pro Val Ser Ile Ser Ile Ala Ala Phe Ala Lys Lys Met
385   390   395   400

Val Thr Thr Lys Glu Lys Pro Asn Pro Phe Ala Cys Ser Tyr Val Ile
                 405   410   415

Val Tyr Ile Asn Ser Gln Phe Pro Gln Val Met Asp Ile Leu Leu Ala
                 420   425   430

Glu Phe His Lys Ala Cys Ile Tyr Thr Val Pro Lys His Ile Val Asn
                 435   440   445

Ser Gln Ser Ala Trp Asp Ser Asp Ala Tyr Glu Arg Leu Asp Ser Ile
         450   455   460

Met Arg Leu Tyr Gly Ala Leu Val Gln Thr Asp Ile Arg Val Gly Asn
465   470   475   480

Ala Thr Asn Val His Gly Ile Glu His Gly Trp Ala Trp Leu Ala Arg
                 485   490   495

Phe Leu Asn Lys Ile Pro Ala Asn Arg Ala Thr Ala Thr Ala Leu Asn
         500   505   510

143

```
Ser Phe Leu Gln Thr Ala Gly Phe Gly Leu His Gln Arg Tyr Lys Ser
        515                 520                 525

Gln Phe Leu Lys Val Val Asn Val Val Arg Glu His Phe Leu Gln Lys
        530                 535                 540

Leu Arg Ala Lys Lys Asp Thr Ser Asp Leu Leu Val Ile Ile Ala Glu
545                 550                 555                 560

Ile Thr Ala Tyr Leu Asp Asp Arg Met Tyr Leu Lys Glu Pro Glu Gly
                565                 570                 575

Arg Ala Met Lys Thr Thr Ser Thr Leu Ser Ser Glu Leu Thr Ala Glu
                580                 585                 590

Leu Asn Gln Pro Asn Tyr Asn Gln Asn Tyr Gln Arg Asn Asp Tyr Arg
        595                 600                 605

Asn Tyr Tyr
    610
```

<210> 63

<211> 1152

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1152)

<223> 38108


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<400> 63
atg gca acg gct tct cct cca ttt atc tca act ctc agc ttc act cac      48
Met Ala Thr Ala Ser Pro Pro Phe Ile Ser Thr Leu Ser Phe Thr His
1               5                   10                  15

tct tct ttc aaa act tct tct tct tct tca ttt tct ccg aag ctt ctt      96
Ser Ser Phe Lys Thr Ser Ser Ser Ser Ser Phe Ser Pro Lys Leu Leu
                20                  25                  30

cga ccc ctc tta agc ttt tcc gtc aaa gct tcc aga aag caa gta gag     144
Arg Pro Leu Leu Ser Phe Ser Val Lys Ala Ser Arg Lys Gln Val Glu
        35                  40                  45
```

144

```
ata gtg ttt gat cct gat gag agg ctt aat aag ata ggt gat gat gtt        192
Ile Val Phe Asp Pro Asp Glu Arg Leu Asn Lys Ile Gly Asp Asp Val
    50                  55                  60

gac aaa gaa gct cct ttg tcc agg ctt aag ctc ttc tca cct tgc aag        240
Asp Lys Glu Ala Pro Leu Ser Arg Leu Lys Leu Phe Ser Pro Cys Lys
65                  70                  75                  80

atc aat gtt ttc ttg agg atc acc gga aag cga gaa gat ggg ttt cat        288
Ile Asn Val Phe Leu Arg Ile Thr Gly Lys Arg Glu Asp Gly Phe His
                85                  90                  95

gat tta gcc tct ttg ttt cat gtg att agc tta gga gac act att aaa        336
Asp Leu Ala Ser Leu Phe His Val Ile Ser Leu Gly Asp Thr Ile Lys
                100                 105                 110

ttc tca ttg tca cca tca aag tct aaa gat cgt ttg tct act aac gtt        384
Phe Ser Leu Ser Pro Ser Lys Ser Lys Asp Arg Leu Ser Thr Asn Val
                115                 120                 125

caa gga gtc cct gtt gat ggg aga aat ctg att ata aaa gca ctt aac        432
Gln Gly Val Pro Val Asp Gly Arg Asn Leu Ile Ile Lys Ala Leu Asn
    130                 135                 140

ctt tac agg aag aaa act ggt agt aac aga ttc ttc tgg att cat tta        480
Leu Tyr Arg Lys Lys Thr Gly Ser Asn Arg Phe Phe Trp Ile His Leu
145                 150                 155                 160

gat aag aag gtg cct acc ggg gct gga ctc ggt ggt gga agt agt aat        528
Asp Lys Lys Val Pro Thr Gly Ala Gly Leu Gly Gly Gly Ser Ser Asn
                165                 170                 175

gct gca act gca ctc tgg gcg gca aat gag ctc aat gga ggt ctt gtc        576
Ala Ala Thr Ala Leu Trp Ala Ala Asn Glu Leu Asn Gly Gly Leu Val
                180                 185                 190

act gag aac gaa ctc cag gat tgg tca agt gaa att ggg tca gat att        624
Thr Glu Asn Glu Leu Gln Asp Trp Ser Ser Glu Ile Gly Ser Asp Ile
                195                 200                 205

cct ttc ttc ttc tcg cat gga gct gcc tat tgt acc ggg aga ggt gag        672
Pro Phe Phe Phe Ser His Gly Ala Ala Tyr Cys Thr Gly Arg Gly Glu
    210                 215                 220

att gtc caa gac ctt cct cca cct ttt cct ctt gat ctt ccg atg gtg        720
Ile Val Gln Asp Leu Pro Pro Pro Phe Pro Leu Asp Leu Pro Met Val
225                 230                 235                 240

ctc ata aag ccc cga gaa gca tgt tcc act gct gaa gtt tac aaa cgt        768
Leu Ile Lys Pro Arg Glu Ala Cys Ser Thr Ala Glu Val Tyr Lys Arg
                245                 250                 255

ctt cgt tta gat cag acg agc aat att aat ccc ttg aca tta cta gag        816
Leu Arg Leu Asp Gln Thr Ser Asn Ile Asn Pro Leu Thr Leu Leu Glu
                260                 265                 270

aat gtg acc agc aat ggt gtg tct caa agc ata tgc gta aac gat ttg        864
Asn Val Thr Ser Asn Gly Val Ser Gln Ser Ile Cys Val Asn Asp Leu
    275                 280                 285
```

145

```
gaa ccg cca gcg ttt tca gtt ctt cca tct cta aaa cgc ttg aag caa      912
Glu Pro Pro Ala Phe Ser Val Leu Pro Ser Leu Lys Arg Leu Lys Gln
    290             295             300

cgg ata ata gca tct gga cgt ggg gaa tac gat gct gtg ttt atg tct      960
Arg Ile Ile Ala Ser Gly Arg Gly Glu Tyr Asp Ala Val Phe Met Ser
305             310             315             320

ggg agt gga agc act att atc ggt att ggt tca cca gat cct cct caa     1008
Gly Ser Gly Ser Thr Ile Ile Gly Ile Gly Ser Pro Asp Pro Pro Gln
            325             330             335

ttt ata tat gat gat gaa gaa tac aag aac gtg ttc ttg tct gaa gca     1056
Phe Ile Tyr Asp Asp Glu Glu Tyr Lys Asn Val Phe Leu Ser Glu Ala
            340             345             350

aac ttt atg acg cgt gag gct aat gaa tgg tac aaa gaa cct gct tct     1104
Asn Phe Met Thr Arg Glu Ala Asn Glu Trp Tyr Lys Glu Pro Ala Ser
        355             360             365

gca aat gct act acc tca tcc gcc gaa tct cgc atg gat ttc caa tga     1152
Ala Asn Ala Thr Thr Ser Ser Ala Glu Ser Arg Met Asp Phe Gln
        370             375             380
```

<210> 64

<211> 383

<212> PRT

<213> Arabidopsis thaliana

<400> 64

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Met Ala Thr Ala Ser Pro Pro Phe Ile Ser Thr Leu Ser Phe Thr His
1               5               10              15


Ser Ser Phe Lys Thr Ser Ser Ser Ser Phe Ser Pro Lys Leu Leu
            20              25              30


Arg Pro Leu Leu Ser Phe Ser Val Lys Ala Ser Arg Lys Gln Val Glu
        35              40              45


Ile Val Phe Asp Pro Asp Glu Arg Leu Asn Lys Ile Gly Asp Asp Val
    50              55              60


Asp Lys Glu Ala Pro Leu Ser Arg Leu Lys Leu Phe Ser Pro Cys Lys
65              70              75              80


Ile Asn Val Phe Leu Arg Ile Thr Gly Lys Arg Glu Asp Gly Phe His
            85              90              95
```

146

Asp Leu Ala Ser Leu Phe His Val Ile Ser Leu Gly Asp Thr Ile Lys
            100   105   110

Phe Ser Leu Ser Pro Ser Lys Ser Lys Asp Arg Leu Ser Thr Asn Val
            115   120   125

Gln Gly Val Pro Val Asp Gly Arg Asn Leu Ile Ile Lys Ala Leu Asn
            130   135   140

Leu Tyr Arg Lys Lys Thr Gly Ser Asn Arg Phe Phe Trp Ile His Leu
145   150   155   160

Asp Lys Lys Val Pro Thr Gly Ala Gly Leu Gly Gly Gly Ser Ser Asn
                165   170   175

Ala Ala Thr Ala Leu Trp Ala Ala Asn Glu Leu Asn Gly Gly Leu Val
            180   185   190

Thr Glu Asn Glu Leu Gln Asp Trp Ser Ser Glu Ile Gly Ser Asp Ile
            195   200   205

Pro Phe Phe Phe Ser His Gly Ala Ala Tyr Cys Thr Gly Arg Gly Glu
    210   215   220

Ile Val Gln Asp Leu Pro Pro Pro Phe Pro Leu Asp Leu Pro Met Val
225   230   235   240

Leu Ile Lys Pro Arg Glu Ala Cys Ser Thr Ala Glu Val Tyr Lys Arg
                245   250   255

Leu Arg Leu Asp Gln Thr Ser Asn Ile Asn Pro Leu Thr Leu Leu Glu
                260   265   270

Asn Val Thr Ser Asn Gly Val Ser Gln Ser Ile Cys Val Asn Asp Leu
            275   280   285

Glu Pro Pro Ala Phe Ser Val Leu Pro Ser Leu Lys Arg Leu Lys Gln
    290   295   300

Arg Ile Ile Ala Ser Gly Arg Gly Glu Tyr Asp Ala Val Phe Met Ser
305   310   315   320

Gly Ser Gly Ser Thr Ile Ile Gly Ile Gly Ser Pro Asp Pro Pro Gln
                325   330   335

147

```
Phe Ile Tyr Asp Asp Glu Glu Tyr Lys Asn Val Phe Leu Ser Glu Ala
        340                 345                 350


Asn Phe Met Thr Arg Glu Ala Asn Glu Trp Tyr Lys Glu Pro Ala Ser
        355                 360                 365


Ala Asn Ala Thr Thr Ser Ser Ala Glu Ser Arg Met Asp Phe Gln
        370                 375                 380
```

<210> 65

<211> 1152

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1152)

<223> 43301


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<400> 65
atg gag gag tca cga gaa tcg ccg gcg gaa cac ggc tac tac atg ccg      48
Met Glu Glu Ser Arg Glu Ser Pro Ala Glu His Gly Tyr Tyr Met Pro
1               5                   10                  15

gcg gaa tgg gat tct cat gct caa act tgg atc ggt tgg cct gaa cgg      96
Ala Glu Trp Asp Ser His Ala Gln Thr Trp Ile Gly Trp Pro Glu Arg
                20                  25                  30

caa gat aac tgg cgg cac aac gct tta ccc gca caa cga gtg ttt gca     144
Gln Asp Asn Trp Arg His Asn Ala Leu Pro Ala Gln Arg Val Phe Ala
        35                  40                  45

gat gtt gca aag gcc atc tca aag ttc gag cct gtc act gtc tgt gct     192
Asp Val Ala Lys Ala Ile Ser Lys Phe Glu Pro Val Thr Val Cys Ala
    50                  55                  60

agc cct gct cag tgg gaa aat gca agg aaa cag ctt cca gag gat ata     240
Ser Pro Ala Gln Trp Glu Asn Ala Arg Lys Gln Leu Pro Glu Asp Ile
65                  70                  75                  80

aga gtt gtt gag atg agc atg aat gat tct tgg ttc cgc gac tct gga     288
Arg Val Val Glu Met Ser Met Asn Asp Ser Trp Phe Arg Asp Ser Gly
                85                  90                  95

cca act ttc att gta cgg aaa aga cca gta aag ctc agt tct ctt aac     336
```

148
```

```
Pro Thr Phe Ile Val Arg Lys Arg Pro Val Lys Leu Ser Ser Leu Asn
        100             105                 110

cga aac att gct ggg atc gac tgg aat ttc aat gcc tgg gga gga gct    384
Arg Asn Ile Ala Gly Ile Asp Trp Asn Phe Asn Ala Trp Gly Gly Ala
        115                 120                 125

aat gat ggc tgt tac aat gat tgg agt cat gac ctt tta gtt tca cga    432
Asn Asp Gly Cys Tyr Asn Asp Trp Ser His Asp Leu Leu Val Ser Arg
        130                 135                 140

aag att ctc gct ttg gaa cga att cca aga ttt caa cat tcg atg att    480
Lys Ile Leu Ala Leu Glu Arg Ile Pro Arg Phe Gln His Ser Met Ile
145             150                 155                 160

ctt gaa gga ggc agc atc cat gtc gat ggg gaa gga acc tgc ctt gtc    528
Leu Glu Gly Gly Ser Ile His Val Asp Gly Glu Gly Thr Cys Leu Val
                165                 170                 175

aca gaa gag tgt ctc ttg aac aaa aac cga aac cct cat atg agt aaa    576
Thr Glu Glu Cys Leu Leu Asn Lys Asn Arg Asn Pro His Met Ser Lys
            180                 185                 190

gag caa ata gag gaa gaa ctt aag aag tac ctc gga gta caa tca ttt    624
Glu Gln Ile Glu Glu Glu Leu Lys Lys Tyr Leu Gly Val Gln Ser Phe
            195                 200                 205

atc tgg ctt cct cgt ggt ctt tac ggg gat gag gac aca aat ggt cac    672
Ile Trp Leu Pro Arg Gly Leu Tyr Gly Asp Glu Asp Thr Asn Gly His
        210                 215                 220

att gat aac atg tgc tgc ttc gct aga ccg gga gtt gtg tta ttg tct    720
Ile Asp Asn Met Cys Cys Phe Ala Arg Pro Gly Val Val Leu Leu Ser
225             230                 235                 240

tgg aca gac gat gaa acc gat cct caa tac gaa agg tct gtg gaa gct    768
Trp Thr Asp Asp Glu Thr Asp Pro Gln Tyr Glu Arg Ser Val Glu Ala
                245                 250                 255

ctt tcg gtt ttg tcg aat tcg att gat gct cgt gga agg aag att caa    816
Leu Ser Val Leu Ser Asn Ser Ile Asp Ala Arg Gly Arg Lys Ile Gln
                260                 265                 270

gtc att aaa ctt tat atc ccg gaa ccc ctt tat atg act gaa gaa gaa    864
Val Ile Lys Leu Tyr Ile Pro Glu Pro Leu Tyr Met Thr Glu Glu Glu
            275                 280                 285

tcg tct gga atc act cag gat ggt gaa gct ata cca aga ctt gca ggg    912
Ser Ser Gly Ile Thr Gln Asp Gly Glu Ala Ile Pro Arg Leu Ala Gly
        290                 295                 300

aca aga ctc gca gca tcg tat gtg aat ttc tac atc gcc aat gga gga    960
Thr Arg Leu Ala Ala Ser Tyr Val Asn Phe Tyr Ile Ala Asn Gly Gly
305             310                 315                 320

ata atc gct cca caa ttc ggt gat cca ata cgt gat aaa gaa gcg att   1008
Ile Ile Ala Pro Gln Phe Gly Asp Pro Ile Arg Asp Lys Glu Ala Ile
                325                 330                 335

cgt gtc ctc tcg gat aca ttt cct cat cac tcg gtt gtg gga atc gag   1056
```

149

```
Arg Val Leu Ser Asp Thr Phe Pro His His Ser Val Val Gly Ile Glu
        340             345                 350

aat gca aga gag atc gtt ctt gct gga gga aac att cat tgt ata acg      1104
Asn Ala Arg Glu Ile Val Leu Ala Gly Gly Asn Ile His Cys Ile Thr
        355             360                 365

cag cag cag ccg gcg gag cct act tcc gtc gcc gaa aat ggc cac tga      1152
Gln Gln Gln Pro Ala Glu Pro Thr Ser Val Ala Glu Asn Gly His
        370             375                 380
```

<210> 66

<211> 383

<212> PRT

<213> Arabidopsis thaliana

<400> 66

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Met Glu Glu Ser Arg Glu Ser Pro Ala Glu His Gly Tyr Tyr Met Pro
1               5                   10                  15


Ala Glu Trp Asp Ser His Ala Gln Thr Trp Ile Gly Trp Pro Glu Arg
            20                  25                  30


Gln Asp Asn Trp Arg His Asn Ala Leu Pro Ala Gln Arg Val Phe Ala
            35                  40                  45


Asp Val Ala Lys Ala Ile Ser Lys Phe Glu Pro Val Thr Val Cys Ala
        50                  55                  60


Ser Pro Ala Gln Trp Glu Asn Ala Arg Lys Gln Leu Pro Glu Asp Ile
65                  70                  75                  80


Arg Val Val Glu Met Ser Met Asn Asp Ser Trp Phe Arg Asp Ser Gly
                85                  90                  95


Pro Thr Phe Ile Val Arg Lys Arg Pro Val Lys Leu Ser Ser Leu Asn
            100                 105                 110


Arg Asn Ile Ala Gly Ile Asp Trp Asn Phe Asn Ala Trp Gly Gly Ala
            115                 120                 125


Asn Asp Gly Cys Tyr Asn Asp Trp Ser His Asp Leu Leu Val Ser Arg
        130                 135                 140
```

Lys Ile Leu Ala Leu Glu Arg Ile Pro Arg Phe Gln His Ser Met Ile
145   150   155   160

Leu Glu Gly Gly Ser Ile His Val Asp Gly Glu Gly Thr Cys Leu Val
                    165   170   175

Thr Glu Glu Cys Leu Leu Asn Lys Asn Arg Asn Pro His Met Ser Lys
                180   185   190

Glu Gln Ile Glu Glu Glu Leu Lys Lys Tyr Leu Gly Val Gln Ser Phe
                195   200   205

Ile Trp Leu Pro Arg Gly Leu Tyr Gly Asp Glu Asp Thr Asn Gly His
    210   215   220

Ile Asp Asn Met Cys Cys Phe Ala Arg Pro Gly Val Val Leu Leu Ser
225   230   235   240

Trp Thr Asp Asp Glu Thr Asp Pro Gln Tyr Glu Arg Ser Val Glu Ala
                245   250   255

Leu Ser Val Leu Ser Asn Ser Ile Asp Ala Arg Gly Arg Lys Ile Gln
                260   265   270

Val Ile Lys Leu Tyr Ile Pro Glu Pro Leu Tyr Met Thr Glu Glu Glu
    275   280   285

Ser Ser Gly Ile Thr Gln Asp Gly Glu Ala Ile Pro Arg Leu Ala Gly
    290   295   300

Thr Arg Leu Ala Ala Ser Tyr Val Asn Phe Tyr Ile Ala Asn Gly Gly
305   310   315   320

Ile Ile Ala Pro Gln Phe Gly Asp Pro Ile Arg Asp Lys Glu Ala Ile
                325   330   335

Arg Val Leu Ser Asp Thr Phe Pro His His Ser Val Val Gly Ile Glu
                340   345   350

Asn Ala Arg Glu Ile Val Leu Ala Gly Gly Asn Ile His Cys Ile Thr
                355   360   365

Gln Gln Gln Pro Ala Glu Pro Thr Ser Val Ala Glu Asn Gly His
                370   375   380

151

<210> 67

<211> 1935

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1935)

<223> 46250

<400> 67

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atg gct agt ctt ctt cga tcc tta atc ctt ttg cta atc gtg caa tca        48
Met Ala Ser Leu Leu Arg Ser Leu Ile Leu Leu Leu Ile Val Gln Ser
1               5                   10                  15

ttt ttg gtt gcg atc gct ttc ggg tcg aaa gaa gtt gaa gaa ttc agc        96
Phe Leu Val Ala Ile Ala Phe Gly Ser Lys Glu Val Glu Glu Phe Ser
                20                  25                  30

gag gca ttg ctc ttg aag cct tta cct gat cga aaa gtt tta gct cac       144
Glu Ala Leu Leu Leu Lys Pro Leu Pro Asp Arg Lys Val Leu Ala His
        35                  40                  45

ttc cac ttc gag aac cga gct cct ccg tca aac tcc cat ggc cgc cat       192
Phe His Phe Glu Asn Arg Ala Pro Pro Ser Asn Ser His Gly Arg His
    50                  55                  60

cac cat ctc ttc ccg aaa gct att tct cag ttg gtt cag aag ttt cgg       240
His His Leu Phe Pro Lys Ala Ile Ser Gln Leu Val Gln Lys Phe Arg
65                  70                  75                  80

gtc aag gag atg gag tta tct ttt act cag ggt cga tgg aac cat gaa       288
Val Lys Glu Met Glu Leu Ser Phe Thr Gln Gly Arg Trp Asn His Glu
                85                  90                  95

cat tgg gga gga ttt gac cct cta tca agt atg aat gcg aag cct gtt       336
His Trp Gly Gly Phe Asp Pro Leu Ser Ser Met Asn Ala Lys Pro Val
            100                 105                 110

ggt gtg gag ctg tgg gct gtg ttt gat gtt cct cag tct cag gtt gat       384
Gly Val Glu Leu Trp Ala Val Phe Asp Val Pro Gln Ser Gln Val Asp
        115                 120                 125

act tct tgg aag aac tta act cat gca ctg tca ggg ctt ttc tgt gct       432
Thr Ser Trp Lys Asn Leu Thr His Ala Leu Ser Gly Leu Phe Cys Ala
        130                 135                 140

tcc atc aat ttt cta gaa tct tcc act tca tat gct gct cct aca tgg       480
Ser Ile Asn Phe Leu Glu Ser Ser Thr Ser Tyr Ala Ala Pro Thr Trp
145                 150                 155                 160
```

```
gga ttt gga ccc aat tct gac aag ctg agg tat ggt tca ctg cca cgt        528
Gly Phe Gly Pro Asn Ser Asp Lys Leu Arg Tyr Gly Ser Leu Pro Arg
                    165               170               175

gaa gct gtt tgt act gag aac ttg acc cca tgg cta aag tta ctt cct        576
Glu Ala Val Cys Thr Glu Asn Leu Thr Pro Trp Leu Lys Leu Leu Pro
                180               185               190

tgt aga gat aag gat ggt att tct gcg tta atg aat agg cca tct gtt        624
Cys Arg Asp Lys Asp Gly Ile Ser Ala Leu Met Asn Arg Pro Ser Val
            195               200               205

tac aga ggg ttt tat cat tct cag aga ttg cat tta tcc acg gtt gaa        672
Tyr Arg Gly Phe Tyr His Ser Gln Arg Leu His Leu Ser Thr Val Glu
        210               215               220

tct ggt caa gag gga ttg ggt tct ggt ata gtg ctg gag cag acg ctt        720
Ser Gly Gln Glu Gly Leu Gly Ser Gly Ile Val Leu Glu Gln Thr Leu
225               230               235               240

act gtt gtt ctt cag cct gag act act tct gtt gaa tca aat atg cag        768
Thr Val Val Leu Gln Pro Glu Thr Thr Ser Val Glu Ser Asn Met Gln
                    245               250               255

cca agt tgg tcc ctc agc tcc ctc ttt ggg aga caa gtt gtt ggg aga        816
Pro Ser Trp Ser Leu Ser Ser Leu Phe Gly Arg Gln Val Val Gly Arg
                260               265               270

tgt gtt ctt gca aag tca agt aat gtg tat ctt caa ttg gaa ggt ctt        864
Cys Val Leu Ala Lys Ser Ser Asn Val Tyr Leu Gln Leu Glu Gly Leu
            275               280               285

ctt ggt tac gaa tca aaa aac gtg gat aca gaa ata gaa gca cac caa        912
Leu Gly Tyr Glu Ser Lys Asn Val Asp Thr Glu Ile Glu Ala His Gln
        290               295               300

cta tgg aag aat gca gag ttt gaa ttg tct ctt aag cca gag agg gtt        960
Leu Trp Lys Asn Ala Glu Phe Glu Leu Ser Leu Lys Pro Glu Arg Val
305               310               315               320

att cga gaa agc tgc agc ttt ctt ttt att ttt gat att gac aaa tca       1008
Ile Arg Glu Ser Cys Ser Phe Leu Phe Ile Phe Asp Ile Asp Lys Ser
                    325               330               335

agt gac agc gag cca ttt gat ctt ggc ctt act tgg aag cgt ccc tca       1056
Ser Asp Ser Glu Pro Phe Asp Leu Gly Leu Thr Trp Lys Arg Pro Ser
                340               345               350

aag tgg tca tgt caa caa gct cca tta cac tcg agt cgg ttt ttg atg       1104
Lys Trp Ser Cys Gln Gln Ala Pro Leu His Ser Ser Arg Phe Leu Met
            355               360               365

gga agc ggg aac gaa aga ggt gca ata gcc atc ttg tta aaa gcg aca       1152
Gly Ser Gly Asn Glu Arg Gly Ala Ile Ala Ile Leu Leu Lys Ala Thr
        370               375               380

gaa tct cag gag aag tta tca ggc aga gat ctc act aat ggc caa tgt       1200
Glu Ser Gln Glu Lys Leu Ser Gly Arg Asp Leu Thr Asn Gly Gln Cys
385               390               395               400
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153

```
aca ata aaa gca aat atc ttc cag att ttc cca tgg tat att aag gtt    1248
Thr Ile Lys Ala Asn Ile Phe Gln Ile Phe Pro Trp Tyr Ile Lys Val
            405                 410                 415

tat tat cat act cta caa atc ttt gtg gat caa caa cag aag aca gac    1296
Tyr Tyr His Thr Leu Gln Ile Phe Val Asp Gln Gln Gln Lys Thr Asp
            420                 425                 430

agt gag gtc tta aag aag atc aat gtc tca cca tct acg gat aag gtg    1344
Ser Glu Val Leu Lys Lys Ile Asn Val Ser Pro Ser Thr Asp Lys Val
            435                 440                 445

tca tct ggc atg atg gag atg atg ttg gaa cta cca tgt gaa gtg aaa    1392
Ser Ser Gly Met Met Glu Met Met Leu Glu Leu Pro Cys Glu Val Lys
        450                 455                 460

tct gta gcc ata tca att gaa tat gat aag ggt ttt ctg cat ata gat    1440
Ser Val Ala Ile Ser Ile Glu Tyr Asp Lys Gly Phe Leu His Ile Asp
465                 470                 475                 480

gaa tat cct cct gat gct aat caa gga ttc gac att cca tcg gct ttg    1488
Glu Tyr Pro Pro Asp Ala Asn Gln Gly Phe Asp Ile Pro Ser Ala Leu
                485                 490                 495

ata agc ttc ccc gat cat cat gct agt tta gat ttc caa gaa gag ctc    1536
Ile Ser Phe Pro Asp His His Ala Ser Leu Asp Phe Gln Glu Glu Leu
                500                 505                 510

agc aac tcg ccc tta tta tca agt tta aag gaa aaa tcc tta gta cgc    1584
Ser Asn Ser Pro Leu Leu Ser Ser Leu Lys Glu Lys Ser Leu Val Arg
            515                 520                 525

tct tac aca gaa gta ttg ctc gta cct ttg aca acc cct gat ttt agc    1632
Ser Tyr Thr Glu Val Leu Leu Val Pro Leu Thr Thr Pro Asp Phe Ser
        530                 535                 540

atg cct tac aac gta atc acg atc aca tgc acc atc ttc gca ttg tat    1680
Met Pro Tyr Asn Val Ile Thr Ile Thr Cys Thr Ile Phe Ala Leu Tyr
545                 550                 555                 560

ttt gga tca ttg cta aat gtt cta cgt aga cga att ggt gaa gaa gaa    1728
Phe Gly Ser Leu Leu Asn Val Leu Arg Arg Arg Ile Gly Glu Glu Glu
                565                 570                 575

agg ttt ctc aaa agc caa gca gga aag aaa aca ggt ggg ctt aag cag    1776
Arg Phe Leu Lys Ser Gln Ala Gly Lys Lys Thr Gly Gly Leu Lys Gln
                580                 585                 590

tta tta tcg aga atc aca gcc aag att aga ggg aga cca att gaa gca    1824
Leu Leu Ser Arg Ile Thr Ala Lys Ile Arg Gly Arg Pro Ile Glu Ala
            595                 600                 605

cca tca tca tca gaa gct gaa tct tcg gtc ttg tct agt aaa ctt atc    1872
Pro Ser Ser Ser Glu Ala Glu Ser Ser Val Leu Ser Ser Lys Leu Ile
        610                 615                 620

tta aaa atc ata tta gtt gca gga gct gct gca gcg tgg caa tat ttt    1920
Leu Lys Ile Ile Leu Val Ala Gly Ala Ala Ala Ala Trp Gln Tyr Phe
625                 630                 635                 640
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tcc acg gac gag tag                                    1935
Ser Thr Asp Glu
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<210> 68

<211> 644

<212> PRT

<213> Arabidopsis thaliana

<400> 68

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Met Ala Ser Leu Leu Arg Ser Leu Ile Leu Leu Ile Val Gln Ser
1                 5                 10                15


Phe Leu Val Ala Ile Ala Phe Gly Ser Lys Glu Val Glu Glu Phe Ser
            20                 25                 30


Glu Ala Leu Leu Leu Lys Pro Leu Pro Asp Arg Lys Val Leu Ala His
            35                 40                 45


Phe His Phe Glu Asn Arg Ala Pro Pro Ser Asn Ser His Gly Arg His
    50                 55                 60


His His Leu Phe Pro Lys Ala Ile Ser Gln Leu Val Gln Lys Phe Arg
65                 70                 75                80


Val Lys Glu Met Glu Leu Ser Phe Thr Gln Gly Arg Trp Asn His Glu
                85                 90                 95


His Trp Gly Gly Phe Asp Pro Leu Ser Ser Met Asn Ala Lys Pro Val
            100                105                110


Gly Val Glu Leu Trp Ala Val Phe Asp Val Pro Gln Ser Gln Val Asp
            115                120                125


Thr Ser Trp Lys Asn Leu Thr His Ala Leu Ser Gly Leu Phe Cys Ala
        130                135                140


Ser Ile Asn Phe Leu Glu Ser Ser Thr Ser Tyr Ala Ala Pro Thr Trp
145                150                155                160


Gly Phe Gly Pro Asn Ser Asp Lys Leu Arg Tyr Gly Ser Leu Pro Arg
                165                170                175
```

Glu Ala Val Cys Thr Glu Asn Leu Thr Pro Trp Leu Lys Leu Leu Pro
              180   185   190

Cys Arg Asp Lys Asp Gly Ile Ser Ala Leu Met Asn Arg Pro Ser Val
              195   200   205

Tyr Arg Gly Phe Tyr His Ser Gln Arg Leu His Leu Ser Thr Val Glu
    210   215   220

Ser Gly Gln Glu Gly Leu Gly Ser Gly Ile Val Leu Glu Gln Thr Leu
225   230   235   240

Thr Val Val Leu Gln Pro Glu Thr Thr Ser Val Glu Ser Asn Met Gln
              245   250   255

Pro Ser Trp Ser Leu Ser Ser Leu Phe Gly Arg Gln Val Val Gly Arg
            260   265   270

Cys Val Leu Ala Lys Ser Ser Asn Val Tyr Leu Gln Leu Glu Gly Leu
        275   280   285

Leu Gly Tyr Glu Ser Lys Asn Val Asp Thr Glu Ile Glu Ala His Gln
    290   295   300

Leu Trp Lys Asn Ala Glu Phe Glu Leu Ser Leu Lys Pro Glu Arg Val
305   310   315   320

Ile Arg Glu Ser Cys Ser Phe Leu Phe Ile Phe Asp Ile Asp Lys Ser
            325   330   335

Ser Asp Ser Glu Pro Phe Asp Leu Gly Leu Thr Trp Lys Arg Pro Ser
            340   345   350

Lys Trp Ser Cys Gln Gln Ala Pro Leu His Ser Ser Arg Phe Leu Met
        355   360   365

Gly Ser Gly Asn Glu Arg Gly Ala Ile Ala Ile Leu Leu Lys Ala Thr
    370   375   380

Glu Ser Gln Glu Lys Leu Ser Gly Arg Asp Leu Thr Asn Gly Gln Cys
385   390   395   400

Thr Ile Lys Ala Asn Ile Phe Gln Ile Phe Pro Trp Tyr Ile Lys Val
            405   410   415

156

Tyr Tyr His Thr Leu Gln Ile Phe Val Asp Gln Gln Gln Lys Thr Asp
            420   425   430

Ser Glu Val Leu Lys Lys Ile Asn Val Ser Pro Ser Thr Asp Lys Val
            435   440   445

Ser Ser Gly Met Met Glu Met Met Leu Glu Leu Pro Cys Glu Val Lys
    450   455   460

Ser Val Ala Ile Ser Ile Glu Tyr Asp Lys Gly Phe Leu His Ile Asp
465   470   475   480

Glu Tyr Pro Pro Asp Ala Asn Gln Gly Phe Asp Ile Pro Ser Ala Leu
                485   490   495

Ile Ser Phe Pro Asp His His Ala Ser Leu Asp Phe Gln Glu Glu Leu
            500   505   510

Ser Asn Ser Pro Leu Leu Ser Ser Leu Lys Glu Lys Ser Leu Val Arg
            515   520   525

Ser Tyr Thr Glu Val Leu Leu Val Pro Leu Thr Thr Pro Asp Phe Ser
    530   535   540

Met Pro Tyr Asn Val Ile Thr Ile Thr Cys Thr Ile Phe Ala Leu Tyr
545   550   555   560

Phe Gly Ser Leu Leu Asn Val Leu Arg Arg Arg Ile Gly Glu Glu Glu
                565   570   575

Arg Phe Leu Lys Ser Gln Ala Gly Lys Lys Thr Gly Gly Leu Lys Gln
            580   585   590

Leu Leu Ser Arg Ile Thr Ala Lys Ile Arg Gly Arg Pro Ile Glu Ala
            595   600   605

Pro Ser Ser Ser Glu Ala Glu Ser Ser Val Leu Ser Ser Lys Leu Ile
    610   615   620

Leu Lys Ile Ile Leu Val Ala Gly Ala Ala Ala Ala Trp Gln Tyr Phe
625   630   635   640

Ser Thr Asp Glu

157

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<210>  69

<211>  210

<212>  DNA

<213>  Arabidopsis thaliana


<220>

<221>  CDS

<222>  (1)..(210)

<223>  47050A


<400>  69
atg ggt gga gga gga cat ggc gga ggt ata act tac aag gga gtc act    48
Met Gly Gly Gly Gly His Gly Gly Gly Ile Thr Tyr Lys Gly Val Thr
1               5                   10                  15

gtc cac act ccc aag act tgg cac acc gtc acc gga aaa ggc ttg tgc    96
Val His Thr Pro Lys Thr Trp His Thr Val Thr Gly Lys Gly Leu Cys
                20                  25                  30

gcc gtt atg tgg ttc tgg att ctg tac agg gca aag caa gat ggt cct   144
Ala Val Met Trp Phe Trp Ile Leu Tyr Arg Ala Lys Gln Asp Gly Pro
            35                  40                  45

gta gtt atg gga tgg agg cac cct tgg gat ggt cat ggt gat cac ggt   192
Val Val Met Gly Trp Arg His Pro Trp Asp Gly His Gly Asp His Gly
        50                  55                  60

cac gga gat cat cac tag                                            210
His Gly Asp His His
65


<210>  70

<211>  69

<212>  PRT

<213>  Arabidopsis thaliana


<400>  70

Met Gly Gly Gly Gly His Gly Gly Gly Ile Thr Tyr Lys Gly Val Thr
1               5                   10                  15
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Val His Thr Pro Lys Thr Trp His Thr Val Thr Gly Lys Gly Leu Cys
              20                  25                  30


Ala Val Met Trp Phe Trp Ile Leu Tyr Arg Ala Lys Gln Asp Gly Pro
          35                  40                  45


Val Val Met Gly Trp Arg His Pro Trp Asp Gly His Gly Asp His Gly
      50                  55                  60


His Gly Asp His His
65
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<210> 71

<211> 978

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(978)

<223> 52949A


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<400> 71
atg gct tct tct tct tgt ttc ctt cgc tcg att ctc ttc tct tct cct    48
Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro
1               5                   10                  15

act aac ctt cgt tca aat cac cat ctc ccc act ttc ttc ccc aag aat    96
Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn
                20                  25                  30

tat ctc att tgc tct cat tcc act tct tct cgc ttc gaa tcg ctc tcg   144
Tyr Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser
            35                  40                  45

gtt tca tcg atc gga act gga tct acc aag aaa tca tcc gat act cgg   192
Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg
        50                  55                  60

aga aag gta aag agc atg gct acg aca aat ata gga aag gag gag aag   240
Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys
65                  70                  75                  80

aaa aga gtc gag att tat gat ctc gaa gag aat tta gtg att gat ttg   288
Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Val Ile Asp Leu
                    85                  90                  95
```

```
gct aaa ttc aca gca gat ctc tcc gat aag ttt tgt aaa gag aga ggc        336
Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly
            100                 105             110

gct ttc acc gtc gtt gtc tcc ggt ggc tct ctc atc aaa tca ctc cgg        384
Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg
            115             120             125

aaa tta gta gaa tct cct tac gtt gat tct ata gat tgg gca agg tgg        432
Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp
        130             135             140

cat ttt ttc tgg gtt gac gag aga gtt gtt ccc aag aat cac gat gat        480
His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp
145             150             155             160

agc aac tat aaa ctc gct tat gat agt ttt cta tcc aag gta cca att        528
Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile
                    165             170             175

ccg cct gga aat gta tat gca atc aac gaa gcc ctc tcc gct gag gct        576
Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala
                180             185             190

gca gcg gat gat tac gag acc tgc ctc aaa cat ttg gtc aac acc aac        624
Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn
            195             200             205

att ctc cgt gta tct gaa tca act ggc ttt ccc aaa ttt gat ctc atg        672
Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met
        210             215             220

ctt cta ggt atg gga cct gat ggt cat gtg gca tca tta ttc cct ggg        720
Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly
225             230             235             240

cat ggt ctc tgc aac gag agc aag aaa tgg gta gtt tca atc tct gac        768
His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp
                245             250             255

tct cca aaa cca ccg tct gag aga atc acc ttc acg ttc ccg gtc atc        816
Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile
                260             265             270

aac tca tct gca cat gta gct cta gtt gtt tgc ggt tct ggg aaa gct        864
Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala
            275             280             285

gaa gct gtg gag gca gct tta aag aag act ggg aat gta cca cct gct        912
Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala
            290             295             300

ggt tct gtt tct gct gaa gac gag ttg gtt tgg ttc ctg gac aaa cca        960
Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro
305             310             315             320

gca tct tcc aag ctc taa        978
Ala Ser Ser Lys Leu
            325
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160

<210> 72

<211> 325

<212> PRT

<213> Arabidopsis thaliana

<400> 72

Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro
1   5   10   15

Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn
            20   25   30

Tyr Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser
        35   40   45

Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg
    50   55   60

Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys
65   70   75   80

Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Val Ile Asp Leu
                85   90   95

Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly
            100   105   110

Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg
            115   120   125

Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp
        130   135   140

His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp
145   150   155   160

Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile
                165   170   175

Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala
            180   185   190

161

```
Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn
        195             200             205

Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met
    210             215             220

Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly
225             230             235             240

His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp
                245             250             255

Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile
            260             265             270

Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala
        275             280             285

Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala
    290             295             300

Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro
305             310             315             320

Ala Ser Ser Lys Leu
                325
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<210> 73

<211> 2343

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2343)

<223> 53210A

<400> 73
atg gct cct gct ttg agt aga agt ctc tac aca tct cct ttg act tca   48

162

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                Met Ala Pro Ala Leu Ser Arg Ser Leu Tyr Thr Ser Pro Leu Thr Ser
                 1               5                   10              15

                gtt cca atc act cct gtc tct tct cgt ctc tct cat ctg aga agc tcg          96
                Val Pro Ile Thr Pro Val Ser Ser Arg Leu Ser His Leu Arg Ser Ser
                            20              25              30

                ttt ctc cca cac ggc ggc gct tta aga acc ggc gtt tcg tgt agc tgg         144
                Phe Leu Pro His Gly Gly Ala Leu Arg Thr Gly Val Ser Cys Ser Trp
                            35              40              45

                aat ctc gaa aag aga tgt aac cga ttc gcc gtg aag tgt gac gcc gcc         192
                Asn Leu Glu Lys Arg Cys Asn Arg Phe Ala Val Lys Cys Asp Ala Ala
                        50              55              60

                gtg gcg gag aaa gag acc act gaa gaa ggg tca ggt gag aag ttt gag         240
                Val Ala Glu Lys Glu Thr Thr Glu Glu Gly Ser Gly Glu Lys Phe Glu
                65                  70              75                  80

                tac caa gct gag gtt agt aga ttg ttg gat ttg att gtt cat agc tta         288
                Tyr Gln Ala Glu Val Ser Arg Leu Leu Asp Leu Ile Val His Ser Leu
                                85              90              95

                tac agt cac aag gag gtg ttt ctc agg gag ctt gta agt aat gca agt         336
                Tyr Ser His Lys Glu Val Phe Leu Arg Glu Leu Val Ser Asn Ala Ser
                            100             105             110

                gat gct ttg gat aag ctg agg ttc ttg agt gta aca gag cct tct ttg         384
                Asp Ala Leu Asp Lys Leu Arg Phe Leu Ser Val Thr Glu Pro Ser Leu
                            115             120             125

                ctt gga gat ggt gga gat ctt gag att agg att aag cct gat cct gat         432
                Leu Gly Asp Gly Gly Asp Leu Glu Ile Arg Ile Lys Pro Asp Pro Asp
                        130             135             140

                aac ggc acc atc acc ata act gat act ggt att gga atg aca aag gaa         480
                Asn Gly Thr Ile Thr Ile Thr Asp Thr Gly Ile Gly Met Thr Lys Glu
                145             150             155             160

                gaa ctt att gat tgc ctt gga act att gct caa agt ggt act tcg aaa         528
                Glu Leu Ile Asp Cys Leu Gly Thr Ile Ala Gln Ser Gly Thr Ser Lys
                            165             170             175

                ttc ttg aag gct cta aag gaa aac aag gac ctt ggt gct gac aac ggt         576
                Phe Leu Lys Ala Leu Lys Glu Asn Lys Asp Leu Gly Ala Asp Asn Gly
                            180             185             190

                ttg atc gga cag ttt ggt gtt ggg ttt tac tct gct ttc tta gtt gct         624
                Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala
                            195             200             205

                gag aag gtt gtt gtg tcc acc aaa agc ccc aaa tct gac aag caa tat         672
                Glu Lys Val Val Val Ser Thr Lys Ser Pro Lys Ser Asp Lys Gln Tyr
                            210             215             220

                gtt tgg gaa tcg gtt gcc gat agt agc tcg tat ctg atc aga gaa gaa         720
                Val Trp Glu Ser Val Ala Asp Ser Ser Ser Tyr Leu Ile Arg Glu Glu
                225                 230             235             240

                aca gac cct gat aac att cta cgt cgt gga aca caa atc acc ttg tat         768
```

163

```
            Thr Asp Pro Asp Asn Ile Leu Arg Arg Gly Thr Gln Ile Thr Leu Tyr
                        245                 250                 255

ctg agg gag gat gat aaa tac gaa ttt gcg gag tct aca agg atc aag          816
Leu Arg Glu Asp Asp Lys Tyr Glu Phe Ala Glu Ser Thr Arg Ile Lys
            260                 265                 270

aac ctc gtg aag aat tac tct cag ttc gtt ggg ttt cct atc tat aca          864
Asn Leu Val Lys Asn Tyr Ser Gln Phe Val Gly Phe Pro Ile Tyr Thr
            275                 280                 285

tgg cag gag aaa tca agg act ata gag gtc gaa gag gac gaa cca gtt          912
Trp Gln Glu Lys Ser Arg Thr Ile Glu Val Glu Glu Asp Glu Pro Val
        290                 295                 300

aag gaa gga gaa gag ggt gag cca aag aaa aag aag acc act aaa act          960
Lys Glu Gly Glu Glu Gly Glu Pro Lys Lys Lys Lys Thr Thr Lys Thr
305                 310                 315                 320

gag aag tat tgg gat tgg gaa cta gcc aac gag acc aaa ccg cta tgg         1008
Glu Lys Tyr Trp Asp Trp Glu Leu Ala Asn Glu Thr Lys Pro Leu Trp
                325                 330                 335

atg cgc aat tcg aag gaa gtg gaa aaa gga gag tac aat gag ttc tac         1056
Met Arg Asn Ser Lys Glu Val Glu Lys Gly Glu Tyr Asn Glu Phe Tyr
            340                 345                 350

aaa aag gct ttc aat gag ttc ttg gat cca ctt gct cac aca cac ttc         1104
Lys Lys Ala Phe Asn Glu Phe Leu Asp Pro Leu Ala His Thr His Phe
            355                 360                 365

aca act gag ggt gag gtt gag ttc agg agc att ttg tac atc cct ggg         1152
Thr Thr Glu Gly Glu Val Glu Phe Arg Ser Ile Leu Tyr Ile Pro Gly
        370                 375                 380

atg ggt cct ctt aac aat gaa gat gtt aca aac ccg aaa aca aag aac         1200
Met Gly Pro Leu Asn Asn Glu Asp Val Thr Asn Pro Lys Thr Lys Asn
385                 390                 395                 400

att cgt ctc tac gtg aag cgt gtg ttt atc tct gac gat ttt gat gga         1248
Ile Arg Leu Tyr Val Lys Arg Val Phe Ile Ser Asp Asp Phe Asp Gly
                405                 410                 415

gag ctt ttc ccg aga tat ctg agc ttt gtg aag gga gtt gtg gac tct         1296
Glu Leu Phe Pro Arg Tyr Leu Ser Phe Val Lys Gly Val Val Asp Ser
                420                 425                 430

gat gat ctt cct ctt aat gtt tct cgt gaa att ctc caa gaa agc aga         1344
Asp Asp Leu Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Glu Ser Arg
            435                 440                 445

att gta aga atc atg aga aag agg ctc att aga aaa acc ttt gac atg         1392
Ile Val Arg Ile Met Arg Lys Arg Leu Ile Arg Lys Thr Phe Asp Met
        450                 455                 460

ata caa gaa atc tct gag agt gaa aac aaa gag gat tac aag aaa ttc         1440
Ile Gln Glu Ile Ser Glu Ser Glu Asn Lys Glu Asp Tyr Lys Lys Phe
465                 470                 475                 480

tgg gag aac ttt ggt aga ttc ctt aaa ttg ggt tgt att gaa gac acc         1488
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```
                  Trp Glu Asn Phe Gly Arg Phe Leu Lys Leu Gly Cys Ile Glu Asp Thr
                                  485                 490                 495

ggt aac cac aag cgt atc aca ccg cta ctt aga ttc ttc agt tcc aag      1536
Gly Asn His Lys Arg Ile Thr Pro Leu Leu Arg Phe Phe Ser Ser Lys
            500                 505                 510

aat gaa gag gaa ttg aca agc ttg gat gat tat atc gag aac atg gga      1584
Asn Glu Glu Glu Leu Thr Ser Leu Asp Asp Tyr Ile Glu Asn Met Gly
            515                 520                 525

gag aac caa aag gcg atc tac tac ctc gca act gat agt ctt aaa agt      1632
Glu Asn Gln Lys Ala Ile Tyr Tyr Leu Ala Thr Asp Ser Leu Lys Ser
    530                 535                 540

gcc aag tct gcc cct ttc ttg gag aaa cta atc caa aaa gat atc gag      1680
Ala Lys Ser Ala Pro Phe Leu Glu Lys Leu Ile Gln Lys Asp Ile Glu
545                 550                 555                 560

gtt cta tat ttg gtt gaa cca atc gat gaa gtt gct att cag aat ttg      1728
Val Leu Tyr Leu Val Glu Pro Ile Asp Glu Val Ala Ile Gln Asn Leu
                565                 570                 575

caa acc tac aaa gaa aag aaa ttc gtt gat atc agt aaa gaa gat ttg      1776
Gln Thr Tyr Lys Glu Lys Lys Phe Val Asp Ile Ser Lys Glu Asp Leu
            580                 585                 590

gaa ctc gga gat gaa gat gaa gta aag gac agg gaa gcg aaa caa gag      1824
Glu Leu Gly Asp Glu Asp Glu Val Lys Asp Arg Glu Ala Lys Gln Glu
            595                 600                 605

ttt aac ctt ctc tgt gac tgg ata aaa cag cag ctc ggt gac aaa gtt      1872
Phe Asn Leu Leu Cys Asp Trp Ile Lys Gln Gln Leu Gly Asp Lys Val
    610                 615                 620

gca aaa gtc caa gtc tca aac cgt ttg agc tct tct cct tgt gtg ctt      1920
Ala Lys Val Gln Val Ser Asn Arg Leu Ser Ser Ser Pro Cys Val Leu
625                 630                 635                 640

gtc tct ggc aaa ttc ggg tgg tca gct aat atg gaa agg cta atg aag      1968
Val Ser Gly Lys Phe Gly Trp Ser Ala Asn Met Glu Arg Leu Met Lys
                645                 650                 655

gca cag gct ctt gga gac act tca agc ctg gag ttc atg aga ggt agg      2016
Ala Gln Ala Leu Gly Asp Thr Ser Ser Leu Glu Phe Met Arg Gly Arg
            660                 665                 670

aga ata cta gag atc aat cca gat cat ccc atc atc aaa gac ttg aac      2064
Arg Ile Leu Glu Ile Asn Pro Asp His Pro Ile Ile Lys Asp Leu Asn
            675                 680                 685

gct gct tgt aag aat gca cca gag agc act gaa gca aca aga gtg gtc      2112
Ala Ala Cys Lys Asn Ala Pro Glu Ser Thr Glu Ala Thr Arg Val Val
            690                 695                 700

gat ctc ttg tat gac act gct ata ata tca agt gga ttc act cct gat      2160
Asp Leu Leu Tyr Asp Thr Ala Ile Ile Ser Ser Gly Phe Thr Pro Asp
705                 710                 715                 720

agc ccg gcc gag ctc ggg aac aag ata tat gag atg atg gca atg gcg      2208
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Ser Pro Ala Glu Leu Gly Asn Lys Ile Tyr Glu Met Met Ala Met Ala
                725   730   735

gtt gga gga aga tgg ggc aga gtt gaa gaa gaa gaa gaa agc tcg act   2256
Val Gly Gly Arg Trp Gly Arg Val Glu Glu Glu Glu Glu Ser Ser Thr
            740   745   750

gtg aat gaa gga gat gac aaa agc gga gaa aca gag gta gtt gaa cca   2304
Val Asn Glu Gly Asp Asp Lys Ser Gly Glu Thr Glu Val Val Glu Pro
        755   760   765

tct gaa gtg agg gca gag agt gat cct tgg caa gat tga   2343
Ser Glu Val Arg Ala Glu Ser Asp Pro Trp Gln Asp
    770   775   780

<210> 74

<211> 780

<212> PRT

<213> Arabidopsis thaliana

<400> 74

Met Ala Pro Ala Leu Ser Arg Ser Leu Tyr Thr Ser Pro Leu Thr Ser
1   5   10   15

Val Pro Ile Thr Pro Val Ser Ser Arg Leu Ser His Leu Arg Ser Ser
            20   25   30

Phe Leu Pro His Gly Gly Ala Leu Arg Thr Gly Val Ser Cys Ser Trp
        35   40   45

Asn Leu Glu Lys Arg Cys Asn Arg Phe Ala Val Lys Cys Asp Ala Ala
    50   55   60

Val Ala Glu Lys Glu Thr Thr Glu Glu Gly Ser Gly Glu Lys Phe Glu
65   70   75   80

Tyr Gln Ala Glu Val Ser Arg Leu Leu Asp Leu Ile Val His Ser Leu
                85   90   95

Tyr Ser His Lys Glu Val Phe Leu Arg Glu Leu Val Ser Asn Ala Ser
            100   105   110

Asp Ala Leu Asp Lys Leu Arg Phe Leu Ser Val Thr Glu Pro Ser Leu
        115   120   125

166

Leu Gly Asp Gly Gly Asp Leu Glu Ile Arg Ile Lys Pro Asp Pro Asp
    130   135   140

Asn Gly Thr Ile Thr Ile Thr Asp Thr Gly Ile Gly Met Thr Lys Glu
145   150   155   160

Glu Leu Ile Asp Cys Leu Gly Thr Ile Ala Gln Ser Gly Thr Ser Lys
                165   170   175

Phe Leu Lys Ala Leu Lys Glu Asn Lys Asp Leu Gly Ala Asp Asn Gly
            180   185   190

Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala
        195   200   205

Glu Lys Val Val Val Ser Thr Lys Ser Pro Lys Ser Asp Lys Gln Tyr
    210   215   220

Val Trp Glu Ser Val Ala Asp Ser Ser Ser Tyr Leu Ile Arg Glu Glu
225   230   235   240

Thr Asp Pro Asp Asn Ile Leu Arg Arg Gly Thr Gln Ile Thr Leu Tyr
            245   250   255

Leu Arg Glu Asp Asp Lys Tyr Glu Phe Ala Glu Ser Thr Arg Ile Lys
        260   265   270

Asn Leu Val Lys Asn Tyr Ser Gln Phe Val Gly Phe Pro Ile Tyr Thr
        275   280   285

Trp Gln Glu Lys Ser Arg Thr Ile Glu Val Glu Glu Asp Glu Pro Val
    290   295   300

Lys Glu Gly Glu Glu Gly Glu Pro Lys Lys Lys Thr Thr Lys Thr
305   310   315   320

Glu Lys Tyr Trp Asp Trp Glu Leu Ala Asn Glu Thr Lys Pro Leu Trp
            325   330   335

Met Arg Asn Ser Lys Glu Val Glu Lys Gly Glu Tyr Asn Glu Phe Tyr
            340   345   350

Lys Lys Ala Phe Asn Glu Phe Leu Asp Pro Leu Ala His Thr His Phe
            355   360   365

167

Thr Thr Glu Gly Glu Val Glu Phe Arg Ser Ile Leu Tyr Ile Pro Gly
    370   375   380

Met Gly Pro Leu Asn Asn Glu Asp Val Thr Asn Pro Lys Thr Lys Asn
385   390   395   400

Ile Arg Leu Tyr Val Lys Arg Val Phe Ile Ser Asp Asp Phe Asp Gly
            405   410   415

Glu Leu Phe Pro Arg Tyr Leu Ser Phe Val Lys Gly Val Val Asp Ser
            420   425   430

Asp Asp Leu Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Glu Ser Arg
        435   440   445

Ile Val Arg Ile Met Arg Lys Arg Leu Ile Arg Lys Thr Phe Asp Met
    450   455   460

Ile Gln Glu Ile Ser Glu Ser Glu Asn Lys Glu Asp Tyr Lys Lys Phe
465   470   475   480

Trp Glu Asn Phe Gly Arg Phe Leu Lys Leu Gly Cys Ile Glu Asp Thr
            485   490   495

Gly Asn His Lys Arg Ile Thr Pro Leu Leu Arg Phe Phe Ser Ser Lys
        500   505   510

Asn Glu Glu Glu Leu Thr Ser Leu Asp Asp Tyr Ile Glu Asn Met Gly
        515   520   525

Glu Asn Gln Lys Ala Ile Tyr Tyr Leu Ala Thr Asp Ser Leu Lys Ser
        530   535   540

Ala Lys Ser Ala Pro Phe Leu Glu Lys Leu Ile Gln Lys Asp Ile Glu
545   550   555   560

Val Leu Tyr Leu Val Glu Pro Ile Asp Glu Val Ala Ile Gln Asn Leu
            565   570   575

Gln Thr Tyr Lys Glu Lys Lys Phe Val Asp Ile Ser Lys Glu Asp Leu
        580   585   590

Glu Leu Gly Asp Glu Asp Glu Val Lys Asp Arg Glu Ala Lys Gln Glu
        595   600   605

168

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Phe Asn Leu Leu Cys Asp Trp Ile Lys Gln Gln Leu Gly Asp Lys Val
    610                 615                 620

Ala Lys Val Gln Val Ser Asn Arg Leu Ser Ser Ser Pro Cys Val Leu
625                 630                 635                 640

Val Ser Gly Lys Phe Gly Trp Ser Ala Asn Met Glu Arg Leu Met Lys
                645                 650                 655

Ala Gln Ala Leu Gly Asp Thr Ser Ser Leu Glu Phe Met Arg Gly Arg
            660                 665                 670

Arg Ile Leu Glu Ile Asn Pro Asp His Pro Ile Ile Lys Asp Leu Asn
        675                 680                 685

Ala Ala Cys Lys Asn Ala Pro Glu Ser Thr Glu Ala Thr Arg Val Val
    690                 695                 700

Asp Leu Leu Tyr Asp Thr Ala Ile Ile Ser Ser Gly Phe Thr Pro Asp
705                 710                 715                 720

Ser Pro Ala Glu Leu Gly Asn Lys Ile Tyr Glu Met Met Ala Met Ala
                725                 730                 735

Val Gly Gly Arg Trp Gly Arg Val Glu Glu Glu Glu Glu Ser Ser Thr
            740                 745                 750

Val Asn Glu Gly Asp Asp Lys Ser Gly Glu Thr Glu Val Val Glu Pro
        755                 760                 765

Ser Glu Val Arg Ala Glu Ser Asp Pro Trp Gln Asp
770                 775                 780
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<210> 75

<211> 2760

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (1)..(2760)

<223> 55483

<400> 75

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Met Asn Met Asn Phe Ser Phe Cys Ser Thr Ser Ser Glu Leu Ser Tyr
1               5                   10                  15

cca agt gag aat gtt ctg aga ttt tct gtt gca agt cgg ctg ttt tct      96
Pro Ser Glu Asn Val Leu Arg Phe Ser Val Ala Ser Arg Leu Phe Ser
                20                  25                  30

cct aaa tgg aag aaa agt ttc att agt tta cct tgt cgt agt aaa act     144
Pro Lys Trp Lys Lys Ser Phe Ile Ser Leu Pro Cys Arg Ser Lys Thr
            35                  40                  45

acg agg aag gtt ttg gcg tca agc cgt tat gtg cca ggg aaa ttg gaa     192
Thr Arg Lys Val Leu Ala Ser Ser Arg Tyr Val Pro Gly Lys Leu Glu
        50                  55                  60

gat ttg tcg gtt gtt aag aag agt tta ccg aga aga gaa cct gtg gag     240
Asp Leu Ser Val Val Lys Lys Ser Leu Pro Arg Arg Glu Pro Val Glu
65                  70                  75                  80

aag ctt ggt ttt gtg agg act ttg ttg att gat aat tat gat agt tat     288
Lys Leu Gly Phe Val Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Tyr
                85                  90                  95

aca ttc aat ata tat cag gct ctg agt act att aat gga gtg cct cct     336
Thr Phe Asn Ile Tyr Gln Ala Leu Ser Thr Ile Asn Gly Val Pro Pro
            100                 105                 110

gtc gtt att cgg aat gat gag tgg acg tgg gaa gaa gct tac cat tac     384
Val Val Ile Arg Asn Asp Glu Trp Thr Trp Glu Glu Ala Tyr His Tyr
        115                 120                 125

tta tat gaa gat gtt gct ttt gat aat att gtt ata tcg cct gga cct     432
Leu Tyr Glu Asp Val Ala Phe Asp Asn Ile Val Ile Ser Pro Gly Pro
        130                 135                 140

ggt tcg cct atg tgt cca gct gat ata gga ata tgt ctt cgt ctt ttg     480
Gly Ser Pro Met Cys Pro Ala Asp Ile Gly Ile Cys Leu Arg Leu Leu
145                 150                 155                 160

ctt gaa tgc cgt gat atc cca att cta ggc gtc tgc ctt ggc cac cag     528
Leu Glu Cys Arg Asp Ile Pro Ile Leu Gly Val Cys Leu Gly His Gln
                165                 170                 175

gca cta ggt tat gtc cat gga gct cat gtg gtg cat gcc ccg gaa cca     576
Ala Leu Gly Tyr Val His Gly Ala His Val Val His Ala Pro Glu Pro
            180                 185                 190

gtc cat gga cgg ttg agt ggg att gaa cat gat ggg aac ata ttg ttt     624
Val His Gly Arg Leu Ser Gly Ile Glu His Asp Gly Asn Ile Leu Phe
        195                 200                 205

tct gat att cca tcc ggg aga aac tct gat ttt aag gtt gtt aga tac     672
Ser Asp Ile Pro Ser Gly Arg Asn Ser Asp Phe Lys Val Val Arg Tyr
        210                 215                 220
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cat tca ctg atc ata gat aag gaa tca cta cca aag gaa ctt gta cca        720
His Ser Leu Ile Ile Asp Lys Glu Ser Leu Pro Lys Glu Leu Val Pro
225                 230                 235                 240

ata gcg tgg acg att tat gat gac act ggc tct ttc tct gag aag aat        768
Ile Ala Trp Thr Ile Tyr Asp Asp Thr Gly Ser Phe Ser Glu Lys Asn
                    245                 250                 255

tcc tgt gtt cct gtg aat aac act ggg agc cca ctt ggg aac gga tct        816
Ser Cys Val Pro Val Asn Asn Thr Gly Ser Pro Leu Gly Asn Gly Ser
                260                 265                 270

gtc att cct gtt tca gaa aag tta gaa aat cga agt cat tgg cct tcg        864
Val Ile Pro Val Ser Glu Lys Leu Glu Asn Arg Ser His Trp Pro Ser
            275                 280                 285

tcc cat gtt aat ggg aaa caa gat aga cac att ctc atg ggc atc atg        912
Ser His Val Asn Gly Lys Gln Asp Arg His Ile Leu Met Gly Ile Met
        290                 295                 300

cat tct tct ttt ccc cat tat ggt tta cag ttt cat cca gaa agt att        960
His Ser Ser Phe Pro His Tyr Gly Leu Gln Phe His Pro Glu Ser Ile
305                 310                 315                 320

gct act acc tat ggt agt cag tta ttt aaa aat ttc aag gac ata act       1008
Ala Thr Thr Tyr Gly Ser Gln Leu Phe Lys Asn Phe Lys Asp Ile Thr
                    325                 330                 335

gtg aat tat tgg agt cgg tgc aaa tct aca tcc ctg cgt cga aga aac       1056
Val Asn Tyr Trp Ser Arg Cys Lys Ser Thr Ser Leu Arg Arg Arg Asn
                    340                 345                 350

ata aat gac act gca aac atg cag gtg cct gat gct act caa ttg ctg       1104
Ile Asn Asp Thr Ala Asn Met Gln Val Pro Asp Ala Thr Gln Leu Leu
                355                 360                 365

aaa gaa ctt tct aga act aga tgt aca gga aat ggt tct agc tat ttt       1152
Lys Glu Leu Ser Arg Thr Arg Cys Thr Gly Asn Gly Ser Ser Tyr Phe
            370                 375                 380

ggg aac cct aag tct ctg ttt tct gcc aag aca aat ggt gta gac gtc       1200
Gly Asn Pro Lys Ser Leu Phe Ser Ala Lys Thr Asn Gly Val Asp Val
385                 390                 395                 400

ttt gat atg gtg gat tca tca tat cca aaa cca cat aca aaa ttg ctg       1248
Phe Asp Met Val Asp Ser Ser Tyr Pro Lys Pro His Thr Lys Leu Leu
                    405                 410                 415

agg ttg aaa tgg aag aag cat gaa cgt ctt gcg cat aaa gtt ggt gga       1296
Arg Leu Lys Trp Lys Lys His Glu Arg Leu Ala His Lys Val Gly Gly
                    420                 425                 430

gta aga aat ata ttt atg gaa ctc ttt ggc aag aat aga gga aat gat       1344
Val Arg Asn Ile Phe Met Glu Leu Phe Gly Lys Asn Arg Gly Asn Asp
                435                 440                 445

act ttt tgg ctg gat act tct tct agt gac aag gct aga gga cga ttt       1392
Thr Phe Trp Leu Asp Thr Ser Ser Ser Asp Lys Ala Arg Gly Arg Phe
            450                 455                 460
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171

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tct ttc atg ggc ggt aaa ggt gga tct ctc tgg aag caa ttg aca ttt      1440
Ser Phe Met Gly Gly Lys Gly Gly Ser Leu Trp Lys Gln Leu Thr Phe
465                 470             475                 480

agt tta tct gat caa agt gag gtt aca tca aaa cat gcg gga cat ctt      1488
Ser Leu Ser Asp Gln Ser Glu Val Thr Ser Lys His Ala Gly His Leu
                    485             490                 495

ctg att gaa gat tct cag agt tct act gag aaa caa ttc ttg gaa gaa      1536
Leu Ile Glu Asp Ser Gln Ser Ser Thr Glu Lys Gln Phe Leu Glu Glu
                500                 505             510

ggc ttt ctt gat ttt ctc cgt aag gag ctt tca tct atc tct tat gat      1584
Gly Phe Leu Asp Phe Leu Arg Lys Glu Leu Ser Ser Ile Ser Tyr Asp
            515                 520             525

gag aag gac ttc gaa gag ttg cct ttt gat ttt tgc ggt gga tac gta      1632
Glu Lys Asp Phe Glu Glu Leu Pro Phe Asp Phe Cys Gly Gly Tyr Val
        530                 535             540

ggt tgt att ggg tat gat att aaa gtg gaa tgt gga atg cca att aat      1680
Gly Cys Ile Gly Tyr Asp Ile Lys Val Glu Cys Gly Met Pro Ile Asn
545                 550             555                 560

cgt cac aaa tcc aac gct cca gat gca tgt ttc ttc ttt gcg gat aat      1728
Arg His Lys Ser Asn Ala Pro Asp Ala Cys Phe Phe Phe Ala Asp Asn
                565                 570             575

gtt gtc gcc att gat cat caa ctc gat gac gtt tat ata tta tcg ctt      1776
Val Val Ala Ile Asp His Gln Leu Asp Asp Val Tyr Ile Leu Ser Leu
            580                 585             590

tac gaa gag gga act gca gaa acc tct ttc ctg aat gat act gaa gag      1824
Tyr Glu Glu Gly Thr Ala Glu Thr Ser Phe Leu Asn Asp Thr Glu Glu
        595                 600             605

aag ctc att agc ttg atg ggt ttg tcc aca aga aag ttg gag gat caa      1872
Lys Leu Ile Ser Leu Met Gly Leu Ser Thr Arg Lys Leu Glu Asp Gln
        610             615                 620

act ctt cca gtt ata gat tca tct caa tcc aaa aca agt ttt gtt cct      1920
Thr Leu Pro Val Ile Asp Ser Ser Gln Ser Lys Thr Ser Phe Val Pro
625                 630             635                 640

gac aaa tcc cga gag cag tat atc aac gat gtt cag agc tgt atg aag      1968
Asp Lys Ser Arg Glu Gln Tyr Ile Asn Asp Val Gln Ser Cys Met Lys
                645                 650             655

tat atc aaa gac ggg gag agc tac gag ctt tgt ctc act act caa aac      2016
Tyr Ile Lys Asp Gly Glu Ser Tyr Glu Leu Cys Leu Thr Thr Gln Asn
                660                 665             670

aga agg aaa ata gga aat gct gat cct ttg gga ctt tat ctc cac ctg      2064
Arg Arg Lys Ile Gly Asn Ala Asp Pro Leu Gly Leu Tyr Leu His Leu
            675                 680             685

aga gag agg aat cca gca cca tat gca gca ttt ctc aac ttc tca aat      2112
Arg Glu Arg Asn Pro Ala Pro Tyr Ala Ala Phe Leu Asn Phe Ser Asn
        690                 695             700
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172

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gca aat ctg tct tta tgc tct tcg tcc cct gaa agg ttt ctt aag ctg      2160
Ala Asn Leu Ser Leu Cys Ser Ser Ser Pro Glu Arg Phe Leu Lys Leu
705             710             715             720

gac aga aat gga atg ctt gaa gca aag ccg att aag ggt act ata gct      2208
Asp Arg Asn Gly Met Leu Glu Ala Lys Pro Ile Lys Gly Thr Ile Ala
                725             730             735

cgt ggc tcc acg cct gaa gaa gat gaa ttt ctt aaa ttg caa ttg aaa      2256
Arg Gly Ser Thr Pro Glu Glu Asp Glu Phe Leu Lys Leu Gln Leu Lys
            740             745             750

ctc agt gag aag aat caa gcc gag aat ctg atg att gtt gac ctt cta      2304
Leu Ser Glu Lys Asn Gln Ala Glu Asn Leu Met Ile Val Asp Leu Leu
            755             760             765

agg aat gat ctc ggt cgt gtc tgt gag cct ggc tca gtc cat gta cct      2352
Arg Asn Asp Leu Gly Arg Val Cys Glu Pro Gly Ser Val His Val Pro
        770             775             780

aac ctc atg gat gta gaa tca tac aca aca gta cat aca atg gtg agc      2400
Asn Leu Met Asp Val Glu Ser Tyr Thr Thr Val His Thr Met Val Ser
785             790             795             800

acg atc cgt gga ctg aaa aaa aca gat att agt cca gtg gaa tgt gta      2448
Thr Ile Arg Gly Leu Lys Lys Thr Asp Ile Ser Pro Val Glu Cys Val
                805             810             815

aga gct gct ttc cct ggc ggt tca atg act ggt gcc cca aaa cta aga      2496
Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly Ala Pro Lys Leu Arg
            820             825             830

tct gtt gag att ctc gat tct cta gag aac tgt tcg aga ggc ctt tac      2544
Ser Val Glu Ile Leu Asp Ser Leu Glu Asn Cys Ser Arg Gly Leu Tyr
            835             840             845

tct ggc tca atc ggg tat ttc tcg tat aat ggt acg ttt gat ctg aat      2592
Ser Gly Ser Ile Gly Tyr Phe Ser Tyr Asn Gly Thr Phe Asp Leu Asn
            850             855             860

att gtg ata aga aca gta ata ata cat gaa gat gaa gct tcc att gga      2640
Ile Val Ile Arg Thr Val Ile Ile His Glu Asp Glu Ala Ser Ile Gly
865             870             875             880

gca gga gga gct att gtt gca tta tca agt cca gaa gat gag ttt gag      2688
Ala Gly Gly Ala Ile Val Ala Leu Ser Ser Pro Glu Asp Glu Phe Glu
                885             890             895

gaa atg att ctt aag act aga gct cct gct aat gca gtc atg gag ttt      2736
Glu Met Ile Leu Lys Thr Arg Ala Pro Ala Asn Ala Val Met Glu Phe
            900             905             910

tgt agt gat cag agg aga caa tag                                      2760
Cys Ser Asp Gln Arg Arg Gln
            915
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<211> 919

<212> PRT

<213> Arabidopsis thaliana

<400> 76

Met Asn Met Asn Phe Ser Phe Cys Ser Thr Ser Ser Glu Leu Ser Tyr
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Pro Ser Glu Asn Val Leu Arg Phe Ser Val Ala Ser Arg Leu Phe Ser
            20   25   30

Pro Lys Trp Lys Lys Ser Phe Ile Ser Leu Pro Cys Arg Ser Lys Thr
        35   40   45

Thr Arg Lys Val Leu Ala Ser Ser Arg Tyr Val Pro Gly Lys Leu Glu
    50   55   60

Asp Leu Ser Val Val Lys Lys Ser Leu Pro Arg Arg Glu Pro Val Glu
65   70   75   80

Lys Leu Gly Phe Val Arg Thr Leu Leu Ile Asp Asn Tyr Asp Ser Tyr
                85   90   95

Thr Phe Asn Ile Tyr Gln Ala Leu Ser Thr Ile Asn Gly Val Pro Pro
                100   105   110

Val Val Ile Arg Asn Asp Glu Trp Thr Trp Glu Glu Ala Tyr His Tyr
            115   120   125

Leu Tyr Glu Asp Val Ala Phe Asp Asn Ile Val Ile Ser Pro Gly Pro
    130   135   140

Gly Ser Pro Met Cys Pro Ala Asp Ile Gly Ile Cys Leu Arg Leu Leu
145   150   155   160

Leu Glu Cys Arg Asp Ile Pro Ile Leu Gly Val Cys Leu Gly His Gln
                165   170   175

Ala Leu Gly Tyr Val His Gly Ala His Val Val His Ala Pro Glu Pro
            180   185   190

Val His Gly Arg Leu Ser Gly Ile Glu His Asp Gly Asn Ile Leu Phe
        195   200   205

Ser Asp Ile Pro Ser Gly Arg Asn Ser Asp Phe Lys Val Val Arg Tyr
    210   215   220

His Ser Leu Ile Ile Asp Lys Glu Ser Leu Pro Lys Glu Leu Val Pro
225   230   235   240

Ile Ala Trp Thr Ile Tyr Asp Asp Thr Gly Ser Phe Ser Glu Lys Asn
                245   250   255

Ser Cys Val Pro Val Asn Asn Thr Gly Ser Pro Leu Gly Asn Gly Ser
                260   265   270

Val Ile Pro Val Ser Glu Lys Leu Glu Asn Arg Ser His Trp Pro Ser
                275   280   285

Ser His Val Asn Gly Lys Gln Asp Arg His Ile Leu Met Gly Ile Met
    290   295   300

His Ser Ser Phe Pro His Tyr Gly Leu Gln Phe His Pro Glu Ser Ile
305   310   315   320

Ala Thr Thr Tyr Gly Ser Gln Leu Phe Lys Asn Phe Lys Asp Ile Thr
                325   330   335

Val Asn Tyr Trp Ser Arg Cys Lys Ser Thr Ser Leu Arg Arg Arg Asn
                340   345   350

Ile Asn Asp Thr Ala Asn Met Gln Val Pro Asp Ala Thr Gln Leu Leu
    355   360   365

Lys Glu Leu Ser Arg Thr Arg Cys Thr Gly Asn Gly Ser Ser Tyr Phe
    370   375   380

Gly Asn Pro Lys Ser Leu Phe Ser Ala Lys Thr Asn Gly Val Asp Val
385   390   395   400

Phe Asp Met Val Asp Ser Ser Tyr Pro Lys Pro His Thr Lys Leu Leu
                405   410   415

Arg Leu Lys Trp Lys Lys His Glu Arg Leu Ala His Lys Val Gly Gly
                420   425   430

Val Arg Asn Ile Phe Met Glu Leu Phe Gly Lys Asn Arg Gly Asn Asp
    435   440   445

175

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Thr Phe Trp Leu Asp Thr Ser Ser Ser Asp Lys Ala Arg Gly Arg Phe
    450               455               460

Ser Phe Met Gly Gly Lys Gly Gly Ser Leu Trp Lys Gln Leu Thr Phe
465               470               475                   480

Ser Leu Ser Asp Gln Ser Glu Val Thr Ser Lys His Ala Gly His Leu
                485               490                   495

Leu Ile Glu Asp Ser Gln Ser Ser Thr Glu Lys Gln Phe Leu Glu Glu
                500               505               510

Gly Phe Leu Asp Phe Leu Arg Lys Glu Leu Ser Ser Ile Ser Tyr Asp
        515               520               525

Glu Lys Asp Phe Glu Glu Leu Pro Phe Asp Phe Cys Gly Gly Tyr Val
    530               535               540

Gly Cys Ile Gly Tyr Asp Ile Lys Val Glu Cys Gly Met Pro Ile Asn
545               550               555                   560

Arg His Lys Ser Asn Ala Pro Asp Ala Cys Phe Phe Phe Ala Asp Asn
                565               570               575

Val Val Ala Ile Asp His Gln Leu Asp Asp Val Tyr Ile Leu Ser Leu
                580               585               590

Tyr Glu Glu Gly Thr Ala Glu Thr Ser Phe Leu Asn Asp Thr Glu Glu
    595               600               605

Lys Leu Ile Ser Leu Met Gly Leu Ser Thr Arg Lys Leu Glu Asp Gln
    610               615               620

Thr Leu Pro Val Ile Asp Ser Ser Gln Ser Lys Thr Ser Phe Val Pro
625               630               635                   640

Asp Lys Ser Arg Glu Gln Tyr Ile Asn Asp Val Gln Ser Cys Met Lys
                645               650               655

Tyr Ile Lys Asp Gly Glu Ser Tyr Glu Leu Cys Leu Thr Thr Gln Asn
                660               665               670

Arg Arg Lys Ile Gly Asn Ala Asp Pro Leu Gly Leu Tyr Leu His Leu
        675               680               685
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176

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Arg Glu Arg Asn Pro Ala Pro Tyr Ala Ala Phe Leu Asn Phe Ser Asn
    690             695             700

Ala Asn Leu Ser Leu Cys Ser Ser Ser Pro Glu Arg Phe Leu Lys Leu
705             710             715             720

Asp Arg Asn Gly Met Leu Glu Ala Lys Pro Ile Lys Gly Thr Ile Ala
            725             730             735

Arg Gly Ser Thr Pro Glu Glu Asp Glu Phe Leu Lys Leu Gln Leu Lys
            740             745             750

Leu Ser Glu Lys Asn Gln Ala Glu Asn Leu Met Ile Val Asp Leu Leu
        755             760             765

Arg Asn Asp Leu Gly Arg Val Cys Glu Pro Gly Ser Val His Val Pro
    770             775             780

Asn Leu Met Asp Val Glu Ser Tyr Thr Thr Val His Thr Met Val Ser
785             790             795             800

Thr Ile Arg Gly Leu Lys Lys Thr Asp Ile Ser Pro Val Glu Cys Val
            805             810             815

Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly Ala Pro Lys Leu Arg
            820             825             830

Ser Val Glu Ile Leu Asp Ser Leu Glu Asn Cys Ser Arg Gly Leu Tyr
        835             840             845

Ser Gly Ser Ile Gly Tyr Phe Ser Tyr Asn Gly Thr Phe Asp Leu Asn
    850             855             860

Ile Val Ile Arg Thr Val Ile Ile His Glu Asp Glu Ala Ser Ile Gly
865             870             875             880

Ala Gly Gly Ala Ile Val Ala Leu Ser Ser Pro Glu Asp Glu Phe Glu
            885             890             895

Glu Met Ile Leu Lys Thr Arg Ala Pro Ala Asn Ala Val Met Glu Phe
        900             905             910

Cys Ser Asp Gln Arg Arg Gln
    915
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<211> 1329

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (1)..(1329)

<223> 58351A

<400> 77

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Met Gly Asp Ser Gly Lys Leu Glu Ala Thr Ile Asp Arg Leu Leu Asn
1               5                   10                  15

gaa gag aag cag atg aga ctc gcc gaa aac gta gcc ggt aca agg aaa    96
Glu Glu Lys Gln Met Arg Leu Ala Glu Asn Val Ala Gly Thr Arg Lys
            20                  25                  30

gcc gcc act gag att ctt cag ctt tgt ttc gat gct aag gat tgg aaa    144
Ala Ala Thr Glu Ile Leu Gln Leu Cys Phe Asp Ala Lys Asp Trp Lys
        35                  40                  45

ctt ctg aat gag cag att ctc aat ctc tct aag aaa cgt ggt cag ctc    192
Leu Leu Asn Glu Gln Ile Leu Asn Leu Ser Lys Lys Arg Gly Gln Leu
    50                  55                  60

aaa cag gct gtg caa tcc atg gtg cag caa gca atg cag tat atc gat    240
Lys Gln Ala Val Gln Ser Met Val Gln Gln Ala Met Gln Tyr Ile Asp
65                  70                  75                  80

cag aca cca gac att gaa act cgg ata gag ctt atc aag acg ctg aac    288
Gln Thr Pro Asp Ile Glu Thr Arg Ile Glu Leu Ile Lys Thr Leu Asn
                85                  90                  95

aat gta tct gct gga aag ata tat gtt gaa atc gag agg gca cgt ctc    336
Asn Val Ser Ala Gly Lys Ile Tyr Val Glu Ile Glu Arg Ala Arg Leu
            100                 105                 110

acc aag aaa ctt gct aag att aag gaa gaa cag ggt cag ata gct gaa    384
Thr Lys Lys Leu Ala Lys Ile Lys Glu Glu Gln Gly Gln Ile Ala Glu
        115                 120                 125

gct gca gat ctt atg caa gaa gtt gct gtg gag aca ttt ggt gct atg    432
Ala Ala Asp Leu Met Gln Glu Val Ala Val Glu Thr Phe Gly Ala Met
    130                 135                 140

gca aaa act gag aaa att gca ttt atc ctt gaa caa gtt cgc ttg tgc    480
```

```
Ala Lys Thr Glu Lys Ile Ala Phe Ile Leu Glu Gln Val Arg Leu Cys
145             150             155             160

ttg gat cgt caa gat ttt gtt cgt gca caa atc tta tct agg aag atc    528
Leu Asp Arg Gln Asp Phe Val Arg Ala Gln Ile Leu Ser Arg Lys Ile
                165             170             175

aat cct aga gtt ttt gac gca gat aca aaa aaa gat aag aag aaa cct    576
Asn Pro Arg Val Phe Asp Ala Asp Thr Lys Lys Asp Lys Lys Lys Pro
            180             185             190

aag gaa ggt gat aac atg gta gaa gag gct cct gct gat ata cca acc    624
Lys Glu Gly Asp Asn Met Val Glu Glu Ala Pro Ala Asp Ile Pro Thr
            195             200             205

ctt ttg gag ctt aag cga att tac tac gag ctt atg att cgg tac tat    672
Leu Leu Glu Leu Lys Arg Ile Tyr Tyr Glu Leu Met Ile Arg Tyr Tyr
    210             215             220

tct cat aac aat gag tac att gaa atc tgc cgt agc tac aag gcg ata    720
Ser His Asn Asn Glu Tyr Ile Glu Ile Cys Arg Ser Tyr Lys Ala Ile
225             230             235             240

tat gat atc cct tca gta aaa gaa act ccg gag cag tgg att ccg gtc    768
Tyr Asp Ile Pro Ser Val Lys Glu Thr Pro Glu Gln Trp Ile Pro Val
                245             250             255

ctg agg aag atc tgc tgg ttc ttg gtc ttg gca cct cat gac cca atg    816
Leu Arg Lys Ile Cys Trp Phe Leu Val Leu Ala Pro His Asp Pro Met
            260             265             270

caa tca agc ttg ctc aat gca act ctg gaa gac aag aat tta tca gaa    864
Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser Glu
            275             280             285

atc cct gat ttc aag atg ctt cta aaa cag gta gtg aca atg gag gtt    912
Ile Pro Asp Phe Lys Met Leu Leu Lys Gln Val Val Thr Met Glu Val
    290             295             300

att caa tgg aca tct ctg tgg aac aaa tac aag gat gag ttc gag aaa    960
Ile Gln Trp Thr Ser Leu Trp Asn Lys Tyr Lys Asp Glu Phe Glu Lys
305             310             315             320

gag aaa agc atg att gga ggt tct ttg ggt gac aaa gct ggt gaa gat   1008
Glu Lys Ser Met Ile Gly Gly Ser Leu Gly Asp Lys Ala Gly Glu Asp
            325             330             335

ctg aaa ctg aga atc atc gaa cat aat atc ctc gtt gtc tca aag tac   1056
Leu Lys Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys Tyr
            340             345             350

tac gca agg ata acc tta aag aga ctt gcc gag ctt tta tgc ctg agc   1104
Tyr Ala Arg Ile Thr Leu Lys Arg Leu Ala Glu Leu Leu Cys Leu Ser
            355             360             365

atg gag gag gcg gag aag cat cta tcg gag atg gta gtg tca aaa gca   1152
Met Glu Glu Ala Glu Lys His Leu Ser Glu Met Val Val Ser Lys Ala
370             375             380

ctg att gca aaa ata gac aga cca tct gga att gtg tgc ttc cag atc   1200
```

179

```
Leu Ile Ala Lys Ile Asp Arg Pro Ser Gly Ile Val Cys Phe Gln Ile
385             390             395             400

gca aag gac agc aac gag att cta aac tcg tgg gca ggg aat ttg gag    1248
Ala Lys Asp Ser Asn Glu Ile Leu Asn Ser Trp Ala Gly Asn Leu Glu
            405             410             415

aag ctt cta gat ctt gtg gaa aag agt tgc cac caa att cac aag gaa    1296
Lys Leu Leu Asp Leu Val Glu Lys Ser Cys His Gln Ile His Lys Glu
            420             425             430

acc atg gtt cac aaa gcc gct ctc aga cct tga                        1329
Thr Met Val His Lys Ala Ala Leu Arg Pro
            435             440
```

<210> 78

<211> 442

<212> PRT

<213> Arabidopsis thaliana

<400> 78

```
Met Gly Asp Ser Gly Lys Leu Glu Ala Thr Ile Asp Arg Leu Leu Asn
1               5               10              15


Glu Glu Lys Gln Met Arg Leu Ala Glu Asn Val Ala Gly Thr Arg Lys
            20              25              30


Ala Ala Thr Glu Ile Leu Gln Leu Cys Phe Asp Ala Lys Asp Trp Lys
        35              40              45


Leu Leu Asn Glu Gln Ile Leu Asn Leu Ser Lys Lys Arg Gly Gln Leu
        50              55              60


Lys Gln Ala Val Gln Ser Met Val Gln Gln Ala Met Gln Tyr Ile Asp
65              70              75              80


Gln Thr Pro Asp Ile Glu Thr Arg Ile Glu Leu Ile Lys Thr Leu Asn
                85              90              95


Asn Val Ser Ala Gly Lys Ile Tyr Val Glu Ile Glu Arg Ala Arg Leu
            100             105             110


Thr Lys Lys Leu Ala Lys Ile Lys Glu Glu Gln Gly Gln Ile Ala Glu
        115             120             125
```

Ala Ala Asp Leu Met Gln Glu Val Ala Val Glu Thr Phe Gly Ala Met
    130   135   140

Ala Lys Thr Glu Lys Ile Ala Phe Ile Leu Glu Gln Val Arg Leu Cys
145   150   155   160

Leu Asp Arg Gln Asp Phe Val Arg Ala Gln Ile Leu Ser Arg Lys Ile
                165   170   175

Asn Pro Arg Val Phe Asp Ala Asp Thr Lys Lys Asp Lys Lys Lys Pro
                180   185   190

Lys Glu Gly Asp Asn Met Val Glu Glu Ala Pro Ala Asp Ile Pro Thr
            195   200   205

Leu Leu Glu Leu Lys Arg Ile Tyr Tyr Glu Leu Met Ile Arg Tyr Tyr
    210   215   220

Ser His Asn Asn Glu Tyr Ile Glu Ile Cys Arg Ser Tyr Lys Ala Ile
225   230   235   240

Tyr Asp Ile Pro Ser Val Lys Glu Thr Pro Glu Gln Trp Ile Pro Val
                245   250   255

Leu Arg Lys Ile Cys Trp Phe Leu Val Leu Ala Pro His Asp Pro Met
                260   265   270

Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser Glu
            275   280   285

Ile Pro Asp Phe Lys Met Leu Leu Lys Gln Val Val Thr Met Glu Val
    290   295   300

Ile Gln Trp Thr Ser Leu Trp Asn Lys Tyr Lys Asp Glu Phe Glu Lys
305   310   315   320

Glu Lys Ser Met Ile Gly Gly Ser Leu Gly Asp Lys Ala Gly Glu Asp
                325   330   335

Leu Lys Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys Tyr
                340   345   350

Tyr Ala Arg Ile Thr Leu Lys Arg Leu Ala Glu Leu Leu Cys Leu Ser
    355   360   365

181

```
Met Glu Glu Ala Glu Lys His Leu Ser Glu Met Val Val Ser Lys Ala
    370                 375             380
```

```
Leu Ile Ala Lys Ile Asp Arg Pro Ser Gly Ile Val Cys Phe Gln Ile
385             390             395                 400
```

```
Ala Lys Asp Ser Asn Glu Ile Leu Asn Ser Trp Ala Gly Asn Leu Glu
            405             410             415
```

```
Lys Leu Leu Asp Leu Val Glu Lys Ser Cys His Gln Ile His Lys Glu
            420             425             430
```

```
Thr Met Val His Lys Ala Ala Leu Arg Pro
        435             440
```

<210> 79

<211> 435

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(435)

<223> 60944

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<400> 79
atg gcg gtt tct ctc ccg aac tcg ttt ctt cag att agc cca tgt gtt      48
Met Ala Val Ser Leu Pro Asn Ser Phe Leu Gln Ile Ser Pro Cys Val
1               5               10              15

cct tct ctg caa tta aga aag ccg gtg atg gcg gca gtg aaa gga gga      96
Pro Ser Leu Gln Leu Arg Lys Pro Val Met Ala Ala Val Lys Gly Gly
            20              25              30

aaa caa tcg gtg aga aga agc agc aat acg gtg gtt cag ata acg tgt     144
Lys Gln Ser Val Arg Arg Ser Ser Asn Thr Val Val Gln Ile Thr Cys
            35              40              45

cgt aag aag gaa ttg cat cct gaa ttc cac gaa gac gca aag gtt tac     192
Arg Lys Lys Glu Leu His Pro Glu Phe His Glu Asp Ala Lys Val Tyr
50              55              60

tgc aat gga gag ctg gtg atg act aca gga gga aca aag aaa gag tat     240
Cys Asn Gly Glu Leu Val Met Thr Thr Gly Gly Thr Lys Lys Glu Tyr
65              70              75              80
```

```
gtg gtt gat gta tgg tca ggt aac cat ccg ttt tac ctc ggg aat cgt      288
Val Val Asp Val Trp Ser Gly Asn His Pro Phe Tyr Leu Gly Asn Arg
                85              90              95

tcg gct ttg atg gtt gat gct gat caa gtt gag aag ttt cgt aag agg      336
Ser Ala Leu Met Val Asp Ala Asp Gln Val Glu Lys Phe Arg Lys Arg
            100             105             110

ttc gct ggg ctt tct gag att atg gag att cct gtg ctt aaa gga gaa      384
Phe Ala Gly Leu Ser Glu Ile Met Glu Ile Pro Val Leu Lys Gly Glu
        115             120             125

atc att atg cct act aag aaa agt aaa ggt ccc aaa ggg aag aag aaa      432
Ile Ile Met Pro Thr Lys Lys Ser Lys Gly Pro Lys Gly Lys Lys Lys
    130             135             140

tga                                                                  435
```

<210> 80

<211> 144

<212> PRT

<213> Arabidopsis thaliana

<400> 80

```
Met Ala Val Ser Leu Pro Asn Ser Phe Leu Gln Ile Ser Pro Cys Val
1               5               10              15

Pro Ser Leu Gln Leu Arg Lys Pro Val Met Ala Ala Val Lys Gly Gly
            20              25              30

Lys Gln Ser Val Arg Arg Ser Ser Asn Thr Val Val Gln Ile Thr Cys
        35              40              45

Arg Lys Lys Glu Leu His Pro Glu Phe His Glu Asp Ala Lys Val Tyr
    50              55              60

Cys Asn Gly Glu Leu Val Met Thr Thr Gly Gly Thr Lys Lys Glu Tyr
65              70              75              80

Val Val Asp Val Trp Ser Gly Asn His Pro Phe Tyr Leu Gly Asn Arg
                85              90              95

Ser Ala Leu Met Val Asp Ala Asp Gln Val Glu Lys Phe Arg Lys Arg
            100             105             110
```

183

```
Phe Ala Gly Leu Ser Glu Ile Met Glu Ile Pro Val Leu Lys Gly Glu
        115                 120                 125


Ile Ile Met Pro Thr Lys Lys Ser Lys Gly Pro Lys Gly Lys Lys Lys
    130                 135                 140
```

<210> 81

<211> 2859

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2859)

<223> 62837


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<400> 81
atg gct tgg tcg ata gct ctt ctt aca cct cct ttt ttt ggt ccc gga        48
Met Ala Trp Ser Ile Ala Leu Leu Thr Pro Pro Phe Phe Gly Pro Gly
1               5                   10                  15

agg cat gtg cag gcc aaa gaa tac agg gaa cca aga ggg tgt gtg atg        96
Arg His Val Gln Ala Lys Glu Tyr Arg Glu Pro Arg Gly Cys Val Met
            20                  25                  30

aag atg agc agt tta aaa gca cct gtt ctg aga att cag gcc aca gaa       144
Lys Met Ser Ser Leu Lys Ala Pro Val Leu Arg Ile Gln Ala Thr Glu
        35                  40                  45

tac aga gaa cca aga ggg cgt gtg aag atg atg tcc agt tta caa gca       192
Tyr Arg Glu Pro Arg Gly Arg Val Lys Met Met Ser Ser Leu Gln Ala
    50                  55                  60

cct ctt ctg aca att cag agc ttc tca ggg tta agg gcc ccc agt gca       240
Pro Leu Leu Thr Ile Gln Ser Phe Ser Gly Leu Arg Ala Pro Ser Ala
65                  70                  75                  80

tta gat tat ttg gga agg cct agt cca ggt ttc ctt gtt aag tat aaa       288
Leu Asp Tyr Leu Gly Arg Pro Ser Pro Gly Phe Leu Val Lys Tyr Lys
                85                  90                  95

ctt gca aaa tca tct ggg aga gaa aaa gct agc cga tgt gta ccc aaa       336
Leu Ala Lys Ser Ser Gly Arg Glu Lys Ala Ser Arg Cys Val Pro Lys
                100                 105                 110

gca atg ttt gag cgt ttt acc gag aaa gca att aag gtc ata atg ctg       384
Ala Met Phe Glu Arg Phe Thr Glu Lys Ala Ile Lys Val Ile Met Leu
            115                 120                 125
```

184

```
tct caa gag gaa gct cgg aga ctt ggc cat aac ttt gtt ggg act gag        432
Ser Gln Glu Glu Ala Arg Arg Leu Gly His Asn Phe Val Gly Thr Glu
    130                 135                 140


caa ata ctg ttg ggt cta att gga gaa ggg act ggg att gcc gcc aag        480
Gln Ile Leu Leu Gly Leu Ile Gly Glu Gly Thr Gly Ile Ala Ala Lys
145                 150                 155                 160


gtt ctt aaa tcc atg ggg atc aat ctt aaa gat tca cgc gtg gaa gta        528
Val Leu Lys Ser Met Gly Ile Asn Leu Lys Asp Ser Arg Val Glu Val
                165                 170                 175


gaa aag ata att ggg aga ggc agt gga ttc gtg gca gtg gag att cca        576
Glu Lys Ile Ile Gly Arg Gly Ser Gly Phe Val Ala Val Glu Ile Pro
                180                 185                 190


ttt act cct cgc gca aag cgg gtg ctg gag ttg tca cta gag gaa gct        624
Phe Thr Pro Arg Ala Lys Arg Val Leu Glu Leu Ser Leu Glu Glu Ala
            195                 200                 205


cga caa ctt ggg cat aac tac att ggt tca gag cac ctt ttg ctt ggt        672
Arg Gln Leu Gly His Asn Tyr Ile Gly Ser Glu His Leu Leu Leu Gly
    210                 215                 220


cta ctt cgt gaa ggg gag ggt gtg gca gct cgt gtc ttg gag aat ttg        720
Leu Leu Arg Glu Gly Glu Gly Val Ala Ala Arg Val Leu Glu Asn Leu
225                 230                 235                 240


ggt gca gat cct agt aat ata cgg aca cag gtt ata cgt atg gtc ggg        768
Gly Ala Asp Pro Ser Asn Ile Arg Thr Gln Val Ile Arg Met Val Gly
                245                 250                 255


gaa aac aat gaa gtc aca gca agc gtt ggt ggg gga agc agc gga aac        816
Glu Asn Asn Glu Val Thr Ala Ser Val Gly Gly Gly Ser Ser Gly Asn
                260                 265                 270


agc aaa atg cca aca ctt gaa gag tat ggg act aac tta act aaa cta        864
Ser Lys Met Pro Thr Leu Glu Glu Tyr Gly Thr Asn Leu Thr Lys Leu
            275                 280                 285


gca gag gag ggt aaa ctg gat ccg gtt gtt gga agg cag cca cag atc        912
Ala Glu Glu Gly Lys Leu Asp Pro Val Val Gly Arg Gln Pro Gln Ile
    290                 295                 300


gaa cga atg gtc cag atc ttg gct cga aga acc aag aac aac cca tgt        960
Glu Arg Met Val Gln Ile Leu Ala Arg Arg Thr Lys Asn Asn Pro Cys
305                 310                 315                 320


ctt att gga gaa cct gga gtt ggt aag acg gca ata gca gaa gga ctt       1008
Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Ile Ala Glu Gly Leu
                325                 330                 335


gca cag cga ata gct agt ggt gat gtt cct gaa aca atc gag ggg aag       1056
Ala Gln Arg Ile Ala Ser Gly Asp Val Pro Glu Thr Ile Glu Gly Lys
            340                 345                 350


acg gtt ata acc ctt gat atg ggt ctt cta gtg gct gga acg aaa tac       1104
Thr Val Ile Thr Leu Asp Met Gly Leu Leu Val Ala Gly Thr Lys Tyr
            355                 360                 365
```

185

```
cgt gga gag ttc gag gaa aga ttg aag aag ctt atg gag gaa atc agg      1152
Arg Gly Glu Phe Glu Glu Arg Leu Lys Lys Leu Met Glu Glu Ile Arg
    370             375             380

caa agt gat gag ata att ctg ttt att gat gaa gtg cac acg ctc atc      1200
Gln Ser Asp Glu Ile Ile Leu Phe Ile Asp Glu Val His Thr Leu Ile
385             390             395             400

ggt gca gga gcc gct gaa ggt gcg atc gat gct gct aac atc tta aag      1248
Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Asn Ile Leu Lys
            405             410             415

cca gct cta gca aga ggt gaa ttg cag tgt att ggt gca aca aca att      1296
Pro Ala Leu Ala Arg Gly Glu Leu Gln Cys Ile Gly Ala Thr Thr Ile
            420             425             430

gat gag tac agg aaa cac att gag aaa gat cct gca ttg gag aga cgg      1344
Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Pro Ala Leu Glu Arg Arg
        435             440             445

ttc cag cct gtg aaa gta cct gaa cca act gta gaa gaa gct ata cag      1392
Phe Gln Pro Val Lys Val Pro Glu Pro Thr Val Glu Glu Ala Ile Gln
    450             455             460

att ttg caa ggt ctg cgt gag cgc tat gag atc cac cac aaa ctt cga      1440
Ile Leu Gln Gly Leu Arg Glu Arg Tyr Glu Ile His His Lys Leu Arg
465             470             475             480

tac act gat gaa gcc ttg gtt gct gct gca caa ttg tca cat cag tac      1488
Tyr Thr Asp Glu Ala Leu Val Ala Ala Ala Gln Leu Ser His Gln Tyr
            485             490             495

atc agt gat cgg ttt ctt ccc gac aaa gcg att gac ttg att gat gaa      1536
Ile Ser Asp Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Glu
            500             505             510

gct ggg tct cgg gtt cga cta cgc cat gct cag ctt cct gag gaa gct      1584
Ala Gly Ser Arg Val Arg Leu Arg His Ala Gln Leu Pro Glu Glu Ala
            515             520             525

aga gag ctt gaa aag caa ctc agg caa atc acc aaa gag aag aat gaa      1632
Arg Glu Leu Glu Lys Gln Leu Arg Gln Ile Thr Lys Glu Lys Asn Glu
    530             535             540

gct gtg cga agc caa gac ttc gag atg gct ggt tct cat cgt gac cgt      1680
Ala Val Arg Ser Gln Asp Phe Glu Met Ala Gly Ser His Arg Asp Arg
545             550             555             560

gaa ata gag ctc aag gct gag ata gct aat gtt tta tct cga ggc aaa      1728
Glu Ile Glu Leu Lys Ala Glu Ile Ala Asn Val Leu Ser Arg Gly Lys
            565             570             575

gaa gtg gcc aaa gcc gag aat gaa gct gag gaa gga gga cct act gtc      1776
Glu Val Ala Lys Ala Glu Asn Glu Ala Glu Glu Gly Gly Pro Thr Val
            580             585             590

aca gaa tct gac atc caa cac atc gtc gcc acc tgg aca gga atc ccg      1824
Thr Glu Ser Asp Ile Gln His Ile Val Ala Thr Trp Thr Gly Ile Pro
            595             600             605
```

186

```
gta gag aaa gtc tcg tct gat gaa tct agc cgt ctt ctc caa atg gag      1872
Val Glu Lys Val Ser Ser Asp Glu Ser Ser Arg Leu Leu Gln Met Glu
        610             615             620

cag acc ctt cac aca aga gtc att ggc caa gat gaa gcc gtt aaa gca      1920
Gln Thr Leu His Thr Arg Val Ile Gly Gln Asp Glu Ala Val Lys Ala
625             630             635             640

atc agt cgg gct atc cgc cgt gcc cgt gtt ggg ctc aaa aac cca aac      1968
Ile Ser Arg Ala Ile Arg Arg Ala Arg Val Gly Leu Lys Asn Pro Asn
            645             650             655

cgt cct atc gcc agt ttc atc ttc tct ggt cca act ggt gtt ggg aaa      2016
Arg Pro Ile Ala Ser Phe Ile Phe Ser Gly Pro Thr Gly Val Gly Lys
            660             665             670

tca gag ctt gct aag gcc ttg gct gct tac tac ttc ggt tca gaa gaa      2064
Ser Glu Leu Ala Lys Ala Leu Ala Ala Tyr Tyr Phe Gly Ser Glu Glu
            675             680             685

gca atg atc cgt ctt gac atg agt gag ttc atg gaa cga cac act gtt      2112
Ala Met Ile Arg Leu Asp Met Ser Glu Phe Met Glu Arg His Thr Val
        690             695             700

tcg aaa ctc atc ggt tca cct cct ggt tac gta gga tac aca gaa gga      2160
Ser Lys Leu Ile Gly Ser Pro Pro Gly Tyr Val Gly Tyr Thr Glu Gly
705             710             715             720

ggt cag tta aca gag gcg gtt cga cgc agg ccc tac act ctt gtt ctc      2208
Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Thr Leu Val Leu
                725             730             735

ttt gac gaa att gag aaa gca cat ccc gat gtt ttc aac atg atg ctt      2256
Phe Asp Glu Ile Glu Lys Ala His Pro Asp Val Phe Asn Met Met Leu
            740             745             750

cag atc cta gaa gac ggt aga cta act gat agc aaa gga aga act gtc      2304
Gln Ile Leu Glu Asp Gly Arg Leu Thr Asp Ser Lys Gly Arg Thr Val
            755             760             765

gat ttc aag aac acg ctt ctg atc atg act tca aac gta ggg agc agc      2352
Asp Phe Lys Asn Thr Leu Leu Ile Met Thr Ser Asn Val Gly Ser Ser
        770             775             780

gtg atc gaa aaa ggt ggt aga aga att ggg ttt gat ctt gac cac gac      2400
Val Ile Glu Lys Gly Gly Arg Arg Ile Gly Phe Asp Leu Asp His Asp
785             790             795             800

gag aaa gac agc agt tac aac aga atc aag agc tta gtg act gag gaa      2448
Glu Lys Asp Ser Ser Tyr Asn Arg Ile Lys Ser Leu Val Thr Glu Glu
                805             810             815

cta aaa cag tat ttc aga cca gag ttc ttg aac agg tta gat gag atg      2496
Leu Lys Gln Tyr Phe Arg Pro Glu Phe Leu Asn Arg Leu Asp Glu Met
            820             825             830

att gtt ttc aga cag tta aca aag ctg gaa gtc aag gag att gct gat      2544
Ile Val Phe Arg Gln Leu Thr Lys Leu Glu Val Lys Glu Ile Ala Asp
            835             840             845
```

187

```
ata atg ctt aaa gaa gtg gtg gcg aga ctt gag gtc aaa gag att gag        2592
Ile Met Leu Lys Glu Val Val Ala Arg Leu Glu Val Lys Glu Ile Glu
        850                 855                 860

ctt cag gtg act gag agg ttt aaa gag aga gtg gtg gat gaa gga ttc        2640
Leu Gln Val Thr Glu Arg Phe Lys Glu Arg Val Val Asp Glu Gly Phe
865                 870                 875                 880

gac ccg agt tat ggt gcg agg cca ctt aga cgt gca ata atg agg ctt        2688
Asp Pro Ser Tyr Gly Ala Arg Pro Leu Arg Arg Ala Ile Met Arg Leu
                885                 890                 895

ttg gag gat agt .atg gcg gag aag atg ctt tca agg gac att aaa gaa       2736
Leu Glu Asp Ser Met Ala Glu Lys Met Leu Ser Arg Asp Ile Lys Glu
                900                 905                 910

gga gat tct gtg att gtt gat gtt gat gcc gaa gga agt gtg gtt gtg        2784
Gly Asp Ser Val Ile Val Asp Val Asp Ala Glu Gly Ser Val Val Val
                915                 920                 925

ttg agt ggt acc act gga cgt gtt ggt ggt ttt gct gct gaa gaa gcc        2832
Leu Ser Gly Thr Thr Gly Arg Val Gly Gly Phe Ala Ala Glu Glu Ala
        930                 935                 940

                                                                       2859
atg gaa gat cct att cca ata ttg tag
Met Glu Asp Pro Ile Pro Ile Leu
945                 950


<210>   82

<211>   952

<212>   PRT

<213>   Arabidopsis thaliana



<400>   82

Met Ala Trp Ser Ile Ala Leu Leu Thr Pro Pro Phe Phe Gly Pro Gly
1                   5                   10                  15


Arg His Val Gln Ala Lys Glu Tyr Arg Glu Pro Arg Gly Cys Val Met
                20                  25                  30


Lys Met Ser Ser Leu Lys Ala Pro Val Leu Arg Ile Gln Ala Thr Glu
        35                  40                  45


Tyr Arg Glu Pro Arg Gly Arg Val Lys Met Met Ser Ser Leu Gln Ala
        50                  55                  60


Pro Leu Leu Thr Ile Gln Ser Phe Ser Gly Leu Arg Ala Pro Ser Ala
65                  70                  75                  .80
```

```
Leu Asp Tyr Leu Gly Arg Pro Ser Pro Gly Phe Leu Val Lys Tyr Lys
             85                  90                  95


Leu Ala Lys Ser Ser Gly Arg Glu Lys Ala Ser Arg Cys Val Pro Lys
            100                 105                 110


Ala Met Phe Glu Arg Phe Thr Glu Lys Ala Ile Lys Val Ile Met Leu
        115                 120                 125


Ser Gln Glu Glu Ala Arg Arg Leu Gly His Asn Phe Val Gly Thr Glu
    130                 135                 140


Gln Ile Leu Leu Gly Leu Ile Gly Glu Gly Thr Gly Ile Ala Ala Lys
145                 150                 155                 160


Val Leu Lys Ser Met Gly Ile Asn Leu Lys Asp Ser Arg Val Glu Val
                165                 170                 175


Glu Lys Ile Ile Gly Arg Gly Ser Gly Phe Val Ala Val Glu Ile Pro
                180                 185                 190


Phe Thr Pro Arg Ala Lys Arg Val Leu Glu Leu Ser Leu Glu Glu Ala
        195                 200                 205


Arg Gln Leu Gly His Asn Tyr Ile Gly Ser Glu His Leu Leu Leu Gly
    210                 215                 220


Leu Leu Arg Glu Gly Glu Gly Val Ala Ala Arg Val Leu Glu Asn Leu
225                 230                 235                 240


Gly Ala Asp Pro Ser Asn Ile Arg Thr Gln Val Ile Arg Met Val Gly
                245                 250                 255


Glu Asn Asn Glu Val Thr Ala Ser Val Gly Gly Gly Ser Ser Gly Asn
            260                 265                 270


Ser Lys Met Pro Thr Leu Glu Glu Tyr Gly Thr Asn Leu Thr Lys Leu
    275                 280                 285


Ala Glu Glu Gly Lys Leu Asp Pro Val Val Gly Arg Gln Pro Gln Ile
    290                 295                 300


Glu Arg Met Val Gln Ile Leu Ala Arg Arg Thr Lys Asn Asn Pro Cys
305                 310                 315                 320
```

189

Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Ile Ala Glu Gly Leu
             325   330   335

Ala Gln Arg Ile Ala Ser Gly Asp Val Pro Glu Thr Ile Glu Gly Lys
             340   345   350

Thr Val Ile Thr Leu Asp Met Gly Leu Leu Val Ala Gly Thr Lys Tyr
             355   360   365

Arg Gly Glu Phe Glu Glu Arg Leu Lys Lys Leu Met Glu Glu Ile Arg
     370   375   380

Gln Ser Asp Glu Ile Ile Leu Phe Ile Asp Glu Val His Thr Leu Ile
385   390   395   400

Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Asn Ile Leu Lys
             405   410   415

Pro Ala Leu Ala Arg Gly Glu Leu Gln Cys Ile Gly Ala Thr Thr Ile
             420   425   430

Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Pro Ala Leu Glu Arg Arg
             435   440   445

Phe Gln Pro Val Lys Val Pro Glu Pro Thr Val Glu Glu Ala Ile Gln
     450   455   460

Ile Leu Gln Gly Leu Arg Glu Arg Tyr Glu Ile His His Lys Leu Arg
465   470   475   480

Tyr Thr Asp Glu Ala Leu Val Ala Ala Ala Gln Leu Ser His Gln Tyr
             485   490   495

Ile Ser Asp Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Glu
             500   505   510

Ala Gly Ser Arg Val Arg Leu Arg His Ala Gln Leu Pro Glu Glu Ala
             515   520   525

Arg Glu Leu Glu Lys Gln Leu Arg Gln Ile Thr Lys Glu Lys Asn Glu
     530   535   540

Ala Val Arg Ser Gln Asp Phe Glu Met Ala Gly Ser His Arg Asp Arg
545   550   555   560

190

Glu Ile Glu Leu Lys Ala Glu Ile Ala Asn Val Leu Ser Arg Gly Lys
              565   570   575

Glu Val Ala Lys Ala Glu Asn Glu Ala Glu Glu Gly Gly Pro Thr Val
              580   585   590

Thr Glu Ser Asp Ile Gln His Ile Val Ala Thr Trp Thr Gly Ile Pro
              595   600   605

Val Glu Lys Val Ser Ser Asp Glu Ser Ser Arg Leu Leu Gln Met Glu
              610   615   620

Gln Thr Leu His Thr Arg Val Ile Gly Gln Asp Glu Ala Val Lys Ala
625   630   635   640

Ile Ser Arg Ala Ile Arg Arg Ala Arg Val Gly Leu Lys Asn Pro Asn
              645   650   655

Arg Pro Ile Ala Ser Phe Ile Phe Ser Gly Pro Thr Gly Val Gly Lys
              660   665   670

Ser Glu Leu Ala Lys Ala Leu Ala Ala Tyr Tyr Phe Gly Ser Glu Glu
              675   680   685

Ala Met Ile Arg Leu Asp Met Ser Glu Phe Met Glu Arg His Thr Val
      690   695   700

Ser Lys Leu Ile Gly Ser Pro Pro Gly Tyr Val Gly Tyr Thr Glu Gly
705   710   715   720

Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Thr Leu Val Leu
              725   730   735

Phe Asp Glu Ile Glu Lys Ala His Pro Asp Val Phe Asn Met Met Leu
              740   745   750

Gln Ile Leu Glu Asp Gly Arg Leu Thr Asp Ser Lys Gly Arg Thr Val
              755   760   765

Asp Phe Lys Asn Thr Leu Leu Ile Met Thr Ser Asn Val Gly Ser Ser
      770   775   780

Val Ile Glu Lys Gly Gly Arg Arg Ile Gly Phe Asp Leu Asp His Asp
785   790   795   800

191

```
Glu Lys Asp Ser Ser Tyr Asn Arg Ile Lys Ser Leu Val Thr Glu Glu
              805                 810             815

Leu Lys Gln Tyr Phe Arg Pro Glu Phe Leu Asn Arg Leu Asp Glu Met
              820             825             830

Ile Val Phe Arg Gln Leu Thr Lys Leu Glu Val Lys Glu Ile Ala Asp
              835             840             845

Ile Met Leu Lys Glu Val Val Ala Arg Leu Glu Val Lys Glu Ile Glu
              850             855             860

Leu Gln Val Thr Glu Arg Phe Lys Glu Arg Val Val Asp Glu Gly Phe
865             870             875             880

Asp Pro Ser Tyr Gly Ala Arg Pro Leu Arg Arg Ala Ile Met Arg Leu
              885             890             895

Leu Glu Asp Ser Met Ala Glu Lys Met Leu Ser Arg Asp Ile Lys Glu
              900             905             910

Gly Asp Ser Val Ile Val Asp Val Asp Ala Glu Gly Ser Val Val Val
              915             920             925

Leu Ser Gly Thr Thr Gly Arg Val Gly Gly Phe Ala Ala Glu Glu Ala
              930             935             940

Met Glu Asp Pro Ile Pro Ile Leu
945             950
```

<210> 83

<211> 1467

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1467)

<223> 65310

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<400>   83
atg act cag gac gtg gag atg aaa gat aac aac acc cct tct caa tcg          48
Met Thr Gln Asp Val Glu Met Lys Asp Asn Asn Thr Pro Ser Gln Ser
1               5                   10                  15


att atc tct tct tct acc tct act atg cag aat ttg aag gag att gca          96
Ile Ile Ser Ser Ser Thr Ser Thr Met Gln Asn Leu Lys Glu Ile Ala
            20                  25                  30


gca ctc atc gat act ggg tct tac acg aag gag gtt cgt cgt att gct         144
Ala Leu Ile Asp Thr Gly Ser Tyr Thr Lys Glu Val Arg Arg Ile Ala
        35                  40                  45


cgt gct gtg cgt ctc act ata ggg ctt agg cag aaa ctc acc ggc tct         192
Arg Ala Val Arg Leu Thr Ile Gly Leu Arg Gln Lys Leu Thr Gly Ser
    50                  55                  60


gtg ctc tct tcc ttc ctg gat ttt gct ttg gtt cca gga tcc gaa gct         240
Val Leu Ser Ser Phe Leu Asp Phe Ala Leu Val Pro Gly Ser Glu Ala
65                  70                  75                  80


cac tct cgc ctc tct tcc ttt gtt cct aag ggt gat gaa cat gac atg         288
His Ser Arg Leu Ser Ser Phe Val Pro Lys Gly Asp Glu His Asp Met
                85                  90                  95


gaa gtt gat act gcc tca tcg gcc aca caa gct gct cct tct aag cat         336
Glu Val Asp Thr Ala Ser Ser Ala Thr Gln Ala Ala Pro Ser Lys His
            100                 105                 110


cta cct gca gag ctc gag atc tac tgc tac ttc att gtt ctt ctt ttt         384
Leu Pro Ala Glu Leu Glu Ile Tyr Cys Tyr Phe Ile Val Leu Leu Phe
        115                 120                 125


ctg att gat cag aag aag tac aac gag gct aaa gct tgt tct tca gca         432
Leu Ile Asp Gln Lys Lys Tyr Asn Glu Ala Lys Ala Cys Ser Ser Ala
    130                 135                 140


agc att gct cgt ctc aag aac gtc aac cga agg acc att gat gtg ata         480
Ser Ile Ala Arg Leu Lys Asn Val Asn Arg Arg Thr Ile Asp Val Ile
145                 150                 155                 160


gca tca aga ctc tac ttt tac tat tct ttg agt tat gag caa acc ggt         528
Ala Ser Arg Leu Tyr Phe Tyr Tyr Ser Leu Ser Tyr Glu Gln Thr Gly
                165                 170                 175


gat ctt gct gaa att cgc ggt act ctt ctt gcg ttg cat cat tct gca         576
Asp Leu Ala Glu Ile Arg Gly Thr Leu Leu Ala Leu His His Ser Ala
            180                 185                 190


acg cta aga cac gat gag ctg ggt cag gaa acc ctt ctg aac ctg ttg         624
Thr Leu Arg His Asp Glu Leu Gly Gln Glu Thr Leu Leu Asn Leu Leu
        195                 200                 205


cta cgt aac tat ttg cat tac aac ctc tat gat cag gca gag aag cta         672
Leu Arg Asn Tyr Leu His Tyr Asn Leu Tyr Asp Gln Ala Glu Lys Leu
    210                 215                 220


aga tca aag gca cct cgc ttt gag gct cat tca aac caa cag ttt tgt         720
```

193

```
Arg Ser Lys Ala Pro Arg Phe Glu Ala His Ser Asn Gln Gln Phe Cys
225             230             235             240

agg tac ctt ttc tat ctc ggg aag att cgt act att cag ctc gaa tat    768
Arg Tyr Leu Phe Tyr Leu Gly Lys Ile Arg Thr Ile Gln Leu Glu Tyr
            245             250             255

acg gac gca aaa gag agc ctt ctt cag gcg gcc agg aaa gcc cct ata    816
Thr Asp Ala Lys Glu Ser Leu Leu Gln Ala Ala Arg Lys Ala Pro Ile
            260             265             270

gca gct ttg ggc ttc agg atc caa tgc aat aaa tgg gca att ctg gtt    864
Ala Ala Leu Gly Phe Arg Ile Gln Cys Asn Lys Trp Ala Ile Leu Val
            275             280             285

cgt cta ctg ctg ggt gag ata cca gag cgt tct atc ttc act caa aag    912
Arg Leu Leu Leu Gly Glu Ile Pro Glu Arg Ser Ile Phe Thr Gln Lys
        290             295             300

ggt atg gag aag gcc ctc aga ccc tac ttc gag cta aca aat gcg gtt    960
Gly Met Glu Lys Ala Leu Arg Pro Tyr Phe Glu Leu Thr Asn Ala Val
305             310             315             320

agg att ggg gac ttg gag ttg ttt agg aca gtc cag gag aag ttc ttg    1008
Arg Ile Gly Asp Leu Glu Leu Phe Arg Thr Val Gln Glu Lys Phe Leu
            325             330             335

gac aca ttt gct caa gac aga acg cac aat ctc atc gtg cga ctc cgc    1056
Asp Thr Phe Ala Gln Asp Arg Thr His Asn Leu Ile Val Arg Leu Arg
            340             345             350

cac aat gtc atc agg act gga ctg cgg aac ata agt atc tcc tac tca    1104
His Asn Val Ile Arg Thr Gly Leu Arg Asn Ile Ser Ile Ser Tyr Ser
            355             360             365

aga atc tct tta ccc gat gtt gcc aaa aag ctg agg ctc aac tct gaa    1152
Arg Ile Ser Leu Pro Asp Val Ala Lys Lys Leu Arg Leu Asn Ser Glu
        370             375             380

aac cct gtg gct gat gcg gaa agc atc gtg gca aag gcc ata cgc gac    1200
Asn Pro Val Ala Asp Ala Glu Ser Ile Val Ala Lys Ala Ile Arg Asp
385             390             395             400

gga gct att gat gct aca atc gat cac aaa aac gga tgc atg gtc tcc    1248
Gly Ala Ile Asp Ala Thr Ile Asp His Lys Asn Gly Cys Met Val Ser
            405             410             415

aaa gaa act ggg gac atc tac tcg acg aat gag cca caa act gcg ttc    1296
Lys Glu Thr Gly Asp Ile Tyr Ser Thr Asn Glu Pro Gln Thr Ala Phe
            420             425             430

aac tca aga att gct ttc tgc ctc aac atg cat aac gaa gct gtc aga    1344
Asn Ser Arg Ile Ala Phe Cys Leu Asn Met His Asn Glu Ala Val Arg
            435             440             445

gca ttg agg ttt cct cct aac act cac aag gag aaa gaa agc gat gag    1392
Ala Leu Arg Phe Pro Pro Asn Thr His Lys Glu Lys Glu Ser Asp Glu
            450             455             460

aag agg aga gag agg aag caa cag gaa gaa gag ctt gct aag cat atg    1440
```

194

```
Lys Arg Arg Glu Arg Lys Gln Gln Glu Glu Glu Leu Ala Lys His Met
465             470             475             480

gct gag gaa gac gat gat gat ttt tag                                    1467
Ala Glu Glu Asp Asp Asp Asp Phe
                485
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<210> 84

<211> 488

<212> PRT

<213> Arabidopsis thaliana

<400> 84

```
Met Thr Gln Asp Val Glu Met Lys Asp Asn Asn Thr Pro Ser Gln Ser
1               5               10              15

Ile Ile Ser Ser Ser Thr Ser Thr Met Gln Asn Leu Lys Glu Ile Ala
            20              25              30

Ala Leu Ile Asp Thr Gly Ser Tyr Thr Lys Glu Val Arg Arg Ile Ala
        35              40              45

Arg Ala Val Arg Leu Thr Ile Gly Leu Arg Gln Lys Leu Thr Gly Ser
    50              55              60

Val Leu Ser Ser Phe Leu Asp Phe Ala Leu Val Pro Gly Ser Glu Ala
65              70              75              80

His Ser Arg Leu Ser Ser Phe Val Pro Lys Gly Asp Glu His Asp Met
                85              90              95

Glu Val Asp Thr Ala Ser Ser Ala Thr Gln Ala Ala Pro Ser Lys His
            100             105             110

Leu Pro Ala Glu Leu Glu Ile Tyr Cys Tyr Phe Ile Val Leu Leu Phe
        115             120             125

Leu Ile Asp Gln Lys Lys Tyr Asn Glu Ala Lys Ala Cys Ser Ser Ala
        130             135             140

Ser Ile Ala Arg Leu Lys Asn Val Asn Arg Arg Thr Ile Asp Val Ile
145             150             155             160
```

Ala Ser Arg Leu Tyr Phe Tyr Tyr Ser Leu Ser Tyr Glu Gln Thr Gly
             165   170   175

Asp Leu Ala Glu Ile Arg Gly Thr Leu Leu Ala Leu His His Ser Ala
             180   185   190

Thr Leu Arg His Asp Glu Leu Gly Gln Glu Thr Leu Leu Asn Leu Leu
             195   200   205

Leu Arg Asn Tyr Leu His Tyr Asn Leu Tyr Asp Gln Ala Glu Lys Leu
     210   215   220

Arg Ser Lys Ala Pro Arg Phe Glu Ala His Ser Asn Gln Gln Phe Cys
225   230   235   240

Arg Tyr Leu Phe Tyr Leu Gly Lys Ile Arg Thr Ile Gln Leu Glu Tyr
             245   250   255

Thr Asp Ala Lys Glu Ser Leu Leu Gln Ala Ala Arg Lys Ala Pro Ile
             260   265   270

Ala Ala Leu Gly Phe Arg Ile Gln Cys Asn Lys Trp Ala Ile Leu Val
             275   280   285

Arg Leu Leu Leu Gly Glu Ile Pro Glu Arg Ser Ile Phe Thr Gln Lys
     290   295   300

Gly Met Glu Lys Ala Leu Arg Pro Tyr Phe Glu Leu Thr Asn Ala Val
305   310   315   320

Arg Ile Gly Asp Leu Glu Leu Phe Arg Thr Val Gln Glu Lys Phe Leu
             325   330   335

Asp Thr Phe Ala Gln Asp Arg Thr His Asn Leu Ile Val Arg Leu Arg
             340   345   350

His Asn Val Ile Arg Thr Gly Leu Arg Asn Ile Ser Ile Ser Tyr Ser
     355   360   365

Arg Ile Ser Leu Pro Asp Val Ala Lys Lys Leu Arg Leu Asn Ser Glu
     370   375   380

Asn Pro Val Ala Asp Ala Glu Ser Ile Val Ala Lys Ala Ile Arg Asp
385   390   395   400

196

```
Gly Ala Ile Asp Ala Thr Ile Asp His Lys Asn Gly Cys Met Val Ser
            405                 410                 415

Lys Glu Thr Gly Asp Ile Tyr Ser Thr Asn Glu Pro Gln Thr Ala Phe
            420                 425                 430

Asn Ser Arg Ile Ala Phe Cys Leu Asn Met His Asn Glu Ala Val Arg
            435                 440                 445

Ala Leu Arg Phe Pro Pro Asn Thr His Lys Glu Lys Glu Ser Asp Glu
    450                 455                 460

Lys Arg Arg Glu Arg Lys Gln Gln Glu Glu Glu Leu Ala Lys His Met
465                 470                 475                 480

Ala Glu Glu Asp Asp Asp Asp Phe
                485
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<210> 85

<211> 282

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(282)

<223> 68181


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<400> 85
atg gac gca agc atg atg gct gga ctt gat ggt ctt cct gaa gaa gac    48
Met Asp Ala Ser Met Met Ala Gly Leu Asp Gly Leu Pro Glu Glu Asp
1               5               10              15

aaa gcc aaa atg gcc tcc atg atc gat cag ctt cag ctc cgt gat agt    96
Lys Ala Lys Met Ala Ser Met Ile Asp Gln Leu Gln Leu Arg Asp Ser
            20              25              30

ttg agg atg tac aat tca ttg gtg gag agg tgt ttc gtg gac tgt gtt   144
Leu Arg Met Tyr Asn Ser Leu Val Glu Arg Cys Phe Val Asp Cys Val
        35              40              45

gat agc ttc aca cgc aaa tct ctg cag aaa caa gag gag act tgt gtg   192
Asp Ser Phe Thr Arg Lys Ser Leu Gln Lys Gln Glu Glu Thr Cys Val
    50              55              60
```

197

```
atg cgt tgc gct gag aag ttc ctt aag cat acg atg cgt gtt ggt atg      240
Met Arg Cys Ala Glu Lys Phe Leu Lys His Thr Met Arg Val Gly Met
65                  70                  75                  80

cgg ttt gct gag ctc aat cag aac gca cca acc caa gac tga              282
Arg Phe Ala Glu Leu Asn Gln Asn Ala Pro Thr Gln Asp
                    85                  90
```

<210> 86

<211> 93

<212> PRT

<213> Arabidopsis thaliana

<400> 86

```
Met Asp Ala Ser Met Met Ala Gly Leu Asp Gly Leu Pro Glu Glu Asp
1               5                   10                  15

Lys Ala Lys Met Ala Ser Met Ile Asp Gln Leu Gln Leu Arg Asp Ser
            20                  25                  30

Leu Arg Met Tyr Asn Ser Leu Val Glu Arg Cys Phe Val Asp Cys Val
        35                  40                  45

Asp Ser Phe Thr Arg Lys Ser Leu Gln Lys Gln Glu Glu Thr Cys Val
    50                  55                  60

Met Arg Cys Ala Glu Lys Phe Leu Lys His Thr Met Arg Val Gly Met
65                  70                  75                  80

Arg Phe Ala Glu Leu Asn Gln Asn Ala Pro Thr Gln Asp
                    85                  90
```

<210> 87

<211> 816

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222>   (1)..(816)

<223>   70913

<400> 87
atg caa tca aaa ccg gga aga gaa aac gaa gag gaa gtc aat aat cac   48
Met Gln Ser Lys Pro Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His
1   5   10   15

cat gct gtt cag cag ccg atg atg tat gca gag ccc tgg tgg aaa aac   96
His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn
            20   25   30

aac tcc ttt ggt gtt gta cct caa gcg aga cct tct gga att cca tca   144
Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser
        35   40   45

aat tcc tct tct ttg gat tgc ccc aat ggt tcc gag tca aac gat gtt   192
Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val
        50   55   60

cat tca gca tct gaa gac ggt gcg ttg aat ggt gaa aac gat ggc act   240
His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr
65   70   75   80

tgg aag gat tca caa gct gca act tcc tct cgt tca gat aat cac gga   288
Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly
                85   90   95

atg gaa gga aat gac cca gcg ctc tct atc cgt aac atg cat gat cag   336
Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln
            100   105   110

cca ctt gta caa cca cca gag ctt gtt gga cac tat atc gct tgt gtc   384
Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val
            115   120   125

cca aac cca tat cag gat cca tat tat ggg gga ttg atg gga gca tat   432
Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr
        130   135   140

ggt cat cag caa ttg ggt ttt cgt cca tat ctt gga atg cct cgt gaa   480
Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu
145   150   155   160

aga aca gct ctg cca ctt gac atg gca caa gag ccc gtt tat gtg aat   528
Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn
                165   170   175

gca aag cag tac gag gga att cta agg cga aga aaa gca cgt gcc aag   576
Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys
            180   185   190

gca gag cta gag agg aaa gtc atc cgg gac aga aag cca tat ctt cac   624
Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His
            195   200   205

gag tca aga cac aag cat gca atg aga agg gca cga gcg agt gga ggc   672

199

```
Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly
    210         215             220

cgg ttt gcg aag aaa agt gag gta gaa gcg gga gag gat gca gga ggg    720
Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly
225             230             235             240

aga gac aga gaa agg ggt tca gca acc aac tca tca ggc tct gaa caa    768
Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln
                245             250             255

gtt gag aca gac tct aat gag acc ctg aat tct tct ggt gca cca taa    816
Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro
            260             265             270
```

<210> 88

<211> 271

<212> PRT

<213> Arabidopsis thaliana

<400> 88

```
Met Gln Ser Lys Pro Gly Arg Glu Asn Glu Glu Glu Val Asn Asn His
1               5               10              15


His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn
            20              25              30


Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser
        35              40              45


Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val
    50              55              60


His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr
65              70              75              80


Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly
                85              90              95


Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln
            100             105             110


Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val
        115             120             125
```

Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr
    130   135   140

Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu
145   150   155   160

Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn
                165   170   175

Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys
                180   185   190

Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His
        195   200   205

Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly
    210   215   220

Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly
225   230   235   240

Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln
                245   250   255

Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro
                260   265   270

<210>   89

<211>   990

<212>   DNA

<213>   Arabidopsis thaliana

<220>

<221>   CDS

<222>   (1)..(990)

<223>   71067

<400>   89
atg agt cgc cgg gtg gaa tac acg tta gct cct ccg cag agg aat gaa   48
Met Ser Arg Arg Val Glu Tyr Thr Leu Ala Pro Pro Gln Arg Asn Glu
1   5   10   15

```
tct gac ggt ttt gat tat ccc gac ggt atc cca ata tca tac aat ctt     96
Ser Asp Gly Phe Asp Tyr Pro Asp Gly Ile Pro Ile Ser Tyr Asn Leu
            20              25              30

cat agg ctt cgt cac ttt gag tgt gaa ggc agt tat ccc aag tat cct    144
His Arg Leu Arg His Phe Glu Cys Glu Gly Ser Tyr Pro Lys Tyr Pro
        35              40              45

tat ggt tct ttg gtc aag ttt tat gca atg gtg gga ctt cat cgt tac    192
Tyr Gly Ser Leu Val Lys Phe Tyr Ala Met Val Gly Leu His Arg Tyr
        50              55              60

aat gtg ttg gag ggg aaa aat ttg cag ctc gat acc cta aag agt ttc    240
Asn Val Leu Glu Gly Lys Asn Leu Gln Leu Asp Thr Leu Lys Ser Phe
65              70              75              80

aac atg aga atc aat tgt ggt gct tct tct tac tac att act ttg gct    288
Asn Met Arg Ile Asn Cys Gly Ala Ser Ser Tyr Tyr Ile Thr Leu Ala
                85              90              95

gca cgc gtt cca gat agc ggt ttg aag cag atc ttt cag gtt cta gtt    336
Ala Arg Val Pro Asp Ser Gly Leu Lys Gln Ile Phe Gln Val Leu Val
            100             105             110

cat gaa gag cgt ctt ggc agt tta gac atg aca tgt act atc gct aga    384
His Glu Glu Arg Leu Gly Ser Leu Asp Met Thr Cys Thr Ile Ala Arg
        115             120             125

cct cga gtg act acc aat gtg cct ttt cta cgt ccg cac agc gaa tca    432
Pro Arg Val Thr Thr Asn Val Pro Phe Leu Arg Pro His Ser Glu Ser
        130             135             140

gag tat gat tat atg gac aat gat gaa ttg cct gac tgg cct tca gag    480
Glu Tyr Asp Tyr Met Asp Asn Asp Glu Leu Pro Asp Trp Pro Ser Glu
145             150             155             160

att gct ttc gat gat aca aaa cgg ttt cat ctg gtg aag gaa tca gag    528
Ile Ala Phe Asp Asp Thr Lys Arg Phe His Leu Val Lys Glu Ser Glu
                165             170             175

ttg cga gac aat gat tgg att cga ctc tat ttg gaa ctt aca ctt gtt    576
Leu Arg Asp Asn Asp Trp Ile Arg Leu Tyr Leu Glu Leu Thr Leu Val
            180             185             190

gct cac gat agg ttt ctt aca gtt cac tat ctc tcc cag ttg gag att    624
Ala His Asp Arg Phe Leu Thr Val His Tyr Leu Ser Gln Leu Glu Ile
        195             200             205

gtg aaa gtt gcg att gaa gaa gtg gag caa ccg aat gcg agt ctc aac    672
Val Lys Val Ala Ile Glu Glu Val Glu Gln Pro Asn Ala Ser Leu Asn
        210             215             220

acc aaa act aca ttt gtc tac ata act tat aag gac ttg gca aag gct    720
Thr Lys Thr Thr Phe Val Tyr Ile Thr Tyr Lys Asp Leu Ala Lys Ala
225             230             235             240

cag att ggt gag ccg gtt gat cgc aaa gct att gtt aga aaa atc atc    768
Gln Ile Gly Glu Pro Val Asp Arg Lys Ala Ile Val Arg Lys Ile Ile
            245             250             255
```

202

```
aat gag act acg gga ctc ttg aga ctc cgg ggt gat tat tgg agt gga        816
Asn Glu Thr Thr Gly Leu Leu Arg Leu Arg Gly Asp Tyr Trp Ser Gly
            260             265             270

gaa aga agt gtg atc act ccg gag gag gaa tat atg ctt ctc cat ggc        864
Glu Arg Ser Val Ile Thr Pro Glu Glu Glu Tyr Met Leu Leu His Gly
            275             280             285

gga gaa aaa gtt cga aac aat gag cag cgt tct aaa aaa ctt aag cgt        912
Gly Glu Lys Val Arg Asn Asn Glu Gln Arg Ser Lys Lys Leu Lys Arg
        290             295             300

cgt gta ggt gtt cat agg cta tgg cga tgg tgg tac cag gct tac aaa        960
Arg Val Gly Val His Arg Leu Trp Arg Trp Trp Tyr Gln Ala Tyr Lys
305             310             315             320

aac cgt ggc ctc cgc tcg tcg tct tat taa                                990
Asn Arg Gly Leu Arg Ser Ser Ser Tyr
            325
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<210> 90

<211> 329

<212> PRT

<213> Arabidopsis thaliana

<400> 90

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Met Ser Arg Arg Val Glu Tyr Thr Leu Ala Pro Pro Gln Arg Asn Glu
1               5               10                  15

Ser Asp Gly Phe Asp Tyr Pro Asp Gly Ile Pro Ile Ser Tyr Asn Leu
            20                  25                  30

His Arg Leu Arg His Phe Glu Cys Glu Gly Ser Tyr Pro Lys Tyr Pro
            35                  40                  45

Tyr Gly Ser Leu Val Lys Phe Tyr Ala Met Val Gly Leu His Arg Tyr
    50                  55                  60

Asn Val Leu Glu Gly Lys Asn Leu Gln Leu Asp Thr Leu Lys Ser Phe
65                  70                  75                  80

Asn Met Arg Ile Asn Cys Gly Ala Ser Ser Tyr Tyr Ile Thr Leu Ala
                85                  90                  95

Ala Arg Val Pro Asp Ser Gly Leu Lys Gln Ile Phe Gln Val Leu Val
            100                 105                 110
```

His Glu Glu Arg Leu Gly Ser Leu Asp Met Thr Cys Thr Ile Ala Arg
         115   120   125

Pro Arg Val Thr Thr Asn Val Pro Phe Leu Arg Pro His Ser Glu Ser
         130   135   140

Glu Tyr Asp Tyr Met Asp Asn Asp Glu Leu Pro Asp Trp Pro Ser Glu
145   150   155   160

Ile Ala Phe Asp Asp Thr Lys Arg Phe His Leu Val Lys Glu Ser Glu
                 165   170   175

Leu Arg Asp Asn Asp Trp Ile Arg Leu Tyr Leu Glu Leu Thr Leu Val
             180   185   190

Ala His Asp Arg Phe Leu Thr Val His Tyr Leu Ser Gln Leu Glu Ile
         195   200   205

Val Lys Val Ala Ile Glu Glu Val Glu Gln Pro Asn Ala Ser Leu Asn
         210   215   220

Thr Lys Thr Thr Phe Val Tyr Ile Thr Tyr Lys Asp Leu Ala Lys Ala
225   230   235   240

Gln Ile Gly Glu Pro Val Asp Arg Lys Ala Ile Val Arg Lys Ile Ile
                 245   250   255

Asn Glu Thr Thr Gly Leu Leu Arg Leu Arg Gly Asp Tyr Trp Ser Gly
             260   265   270

Glu Arg Ser Val Ile Thr Pro Glu Glu Glu Tyr Met Leu Leu His Gly
         275   280   285

Gly Glu Lys Val Arg Asn Asn Glu Gln Arg Ser Lys Lys Leu Lys Arg
         290   295   300

Arg Val Gly Val His Arg Leu Trp Arg Trp Trp Tyr Gln Ala Tyr Lys
305   310   315   320

Asn Arg Gly Leu Arg Ser Ser Ser Tyr
                 325

<210>   91

204

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<211>   1614

<212>   DNA

<213>   Arabidopsis thaliana


<220>

<221>   CDS

<222>   (1)..(1614)

<223>   71654


<400>   91
atg gcg ctc gtg aaa acg gaa acg cag gcg tta gga aac cac cag cat      48
Met Ala Leu Val Lys Thr Glu Thr Gln Ala Leu Gly Asn His Gln His
1                5                  10                  15

tct tca agg ttt ggt tcg ctt tac gtc ggt gat ctt agc cca gac gtg      96
Ser Ser Arg Phe Gly Ser Leu Tyr Val Gly Asp Leu Ser Pro Asp Val
                20                  25                  30

acg gag aaa gat ctc att gat aag ttc tct ttg aat gtt ccg gta gtg     144
Thr Glu Lys Asp Leu Ile Asp Lys Phe Ser Leu Asn Val Pro Val Val
            35                  40                  45

tcc gtt cat ctt tgc cgt aac tct gtc acc gga aaa tcc atg tgt tac     192
Ser Val His Leu Cys Arg Asn Ser Val Thr Gly Lys Ser Met Cys Tyr
        50                  55                  60

gct tac atc aac ttc gat tca cct ttc agc gca tcg aat gct atg act     240
Ala Tyr Ile Asn Phe Asp Ser Pro Phe Ser Ala Ser Asn Ala Met Thr
65                  70                  75                  80

cgc tta aac cat agt gat ttg aag gga aag gct atg cga ata atg tgg     288
Arg Leu Asn His Ser Asp Leu Lys Gly Lys Ala Met Arg Ile Met Trp
                85                  90                  95

tct cag agg gat ctt gcg tac cgt cgt cgt act cgt act ggt ttt gca     336
Ser Gln Arg Asp Leu Ala Tyr Arg Arg Arg Thr Arg Thr Gly Phe Ala
            100                 105                 110

aat cta tac gta aag aat ctg gat agc tcg att act agc agt tgc tta     384
Asn Leu Tyr Val Lys Asn Leu Asp Ser Ser Ile Thr Ser Ser Cys Leu
            115                 120                 125

gag cga atg ttt tgc ccc ttt ggt tcc ata ctt tct tgc aaa gtc gtt     432
Glu Arg Met Phe Cys Pro Phe Gly Ser Ile Leu Ser Cys Lys Val Val
        130                 135                 140

gaa gag aat ggc caa agt aaa ggt ttt ggc ttt gtt cag ttt gat aca     480
Glu Glu Asn Gly Gln Ser Lys Gly Phe Gly Phe Val Gln Phe Asp Thr
145                 150                 155                 160

gag caa tct gct gta tct gct cgt tct gct ctc cac ggc tct atg gtt     528
```

```
Glu Gln Ser Ala Val Ser Ala Arg Ser Ala Leu His Gly Ser Met Val
             165                 170                 175

tat ggc aag aaa ctg ttt gtt gcc aag ttc atc aac aag gat gaa aga    576
Tyr Gly Lys Lys Leu Phe Val Ala Lys Phe Ile Asn Lys Asp Glu Arg
             180                 185                 190

gca gct atg gca gga aat caa gac tct aca aac gtt tat gtg aag aat    624
Ala Ala Met Ala Gly Asn Gln Asp Ser Thr Asn Val Tyr Val Lys Asn
             195                 200                 205

ctg atc gaa act gtt aca gat gat tgt cta cat aca ctg ttt tct caa    672
Leu Ile Glu Thr Val Thr Asp Asp Cys Leu His Thr Leu Phe Ser Gln
210                 215                 220

tat gga act gtc tct agt gtt gtg gtt atg agg gat ggt atg gga aga    720
Tyr Gly Thr Val Ser Ser Val Val Val Met Arg Asp Gly Met Gly Arg
225                 230                 235                 240

tct aga ggt ttc gga ttt gtt aac ttc tgc aat cca gaa aat gct aag    768
Ser Arg Gly Phe Gly Phe Val Asn Phe Cys Asn Pro Glu Asn Ala Lys
                 245                 250                 255

aaa gct atg gaa tct ctc tgt gga cta caa ctt gga tcg aag aaa ttg    816
Lys Ala Met Glu Ser Leu Cys Gly Leu Gln Leu Gly Ser Lys Lys Leu
             260                 265                 270

ttt gtt ggt aag gca ctc aag aaa gat gaa agg agg gag atg ctg aaa    864
Phe Val Gly Lys Ala Leu Lys Lys Asp Glu Arg Arg Glu Met Leu Lys
             275                 280                 285

cag aaa ttc agt gac aac ttt att gca aag cct aac atg aga tgg tcc    912
Gln Lys Phe Ser Asp Asn Phe Ile Ala Lys Pro Asn Met Arg Trp Ser
290                 295                 300

aat ctg tac gtg aag aac ttg agt gaa tca atg aat gaa aca aga ctg    960
Asn Leu Tyr Val Lys Asn Leu Ser Glu Ser Met Asn Glu Thr Arg Leu
305                 310                 315                 320

cga gaa atc ttt gga tgc tat ggg caa ata gtt tca gct aaa gtg atg   1008
Arg Glu Ile Phe Gly Cys Tyr Gly Gln Ile Val Ser Ala Lys Val Met
                 325                 330                 335

tgt cat gag aat ggc aga agt aaa gga ttc ggc ttt gtg tgc ttc tct   1056
Cys His Glu Asn Gly Arg Ser Lys Gly Phe Gly Phe Val Cys Phe Ser
             340                 345                 350

aac tgt gaa gag tcc aaa cag gct aaa aga tat ctc aat ggg ttc tta   1104
Asn Cys Glu Glu Ser Lys Gln Ala Lys Arg Tyr Leu Asn Gly Phe Leu
             355                 360                 365

gtt gat gga aag cca ata gtt gtt cga gtt gca gag cgc aaa gag gat   1152
Val Asp Gly Lys Pro Ile Val Val Arg Val Ala Glu Arg Lys Glu Asp
370                 375                 380

cga atc aag agg ttg cag caa tat ttt cag gca cag cca cgc cag tac   1200
Arg Ile Lys Arg Leu Gln Gln Tyr Phe Gln Ala Gln Pro Arg Gln Tyr
385                 390                 395                 400

acg caa gct cct tct gcc cct tca cca gct cag cca gtc ctc tca tat   1248
```

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Thr Gln Ala Pro Ser Ala Pro Ser Pro Ala Gln Pro Val Leu Ser Tyr
            405             ·410                     415

gtg tcc agc tca tat ggt tgc ttt cag cca ttc cag gtc ggg aca tct     1296
Val Ser Ser Ser Tyr Gly Cys Phe Gln Pro Phe Gln Val Gly Thr Ser
            420             425             430

tat tac tat atg ggc aat cag gtg cca caa atg tcc ggt cac caa aac     1344
Tyr Tyr Tyr Met Gly Asn Gln Val Pro Gln Met Ser Gly His Gln Asn
            435             440             445

atc acc acc tac gtt cca gct ggg aaa gtg cct ctc aag gag aga aga     1392
Ile Thr Thr Tyr Val Pro Ala Gly Lys Val Pro Leu Lys Glu Arg Arg
        450             455             460

tca atg cat ctg gtc tac aaa cat ccg gct tat ccc gtt gcc aag agg     1440
Ser Met His Leu Val Tyr Lys His Pro Ala Tyr Pro Val Ala Lys Arg
465             470             475             480

ggt gct aaa cag aca ctg gtt ttt aag ggt gag gtt aac aga aat tta     1488
Gly Ala Lys Gln Thr Leu Val Phe Lys Gly Glu Val Asn Arg Asn Leu
            485             490             495

gag gct gca aca tgc tcc aaa gca aca aca tct gag gag aac cgt aaa     1536
Glu Ala Ala Thr Cys Ser Lys Ala Thr Thr Ser Glu Glu Asn Arg Lys
        500             505             510

gaa gaa cga aga ttg act ttg tca gga aag ttg tca cca gaa gtg aag     1584
Glu Glu Arg Arg Leu Thr Leu Ser Gly Lys Leu Ser Pro Glu Val Lys
    ·   515             520             525

gta gag gaa tca gga aaa caa ttg caa tga                             1614
Val Glu Glu Ser Gly Lys Gln Leu Gln
    530             535
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<210> 92

<211> 537

<212> PRT

<213> Arabidopsis thaliana

<400> 92

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Met Ala Leu Val Lys Thr Glu Thr Gln Ala Leu Gly Asn His Gln His
.1               5                   10                  15


Ser Ser Arg Phe Gly Ser Leu Tyr Val Gly Asp Leu Ser Pro Asp Val
            20                  25                  30


Thr Glu Lys Asp Leu Ile Asp Lys Phe Ser Leu Asn Val Pro Val Val
            35                  40                  45
```

Ser Val His Leu Cys Arg Asn Ser Val Thr Gly Lys Ser Met Cys Tyr
    50   55   60

Ala Tyr Ile Asn Phe Asp Ser Pro Phe Ser Ala Ser Asn Ala Met Thr
65   70   75   80

Arg Leu Asn His Ser Asp Leu Lys Gly Lys Ala Met Arg Ile Met Trp
            85   90   95

Ser Gln Arg Asp Leu Ala Tyr Arg Arg Arg Thr Arg Thr Gly Phe Ala
            100   105   110

Asn Leu Tyr Val Lys Asn Leu Asp Ser Ser Ile Thr Ser Ser Cys Leu
        115   120   125   .

Glu Arg Met Phe Cys Pro Phe Gly Ser Ile Leu Ser Cys Lys Val Val
    130   135   140

Glu Glu Asn Gly Gln Ser Lys Gly Phe Gly Phe Val Gln Phe Asp Thr
145   150   155   160

Glu Gln Ser Ala Val Ser Ala Arg Ser Ala Leu His Gly Ser Met Val
            165   170   175

Tyr Gly Lys Lys Leu Phe Val Ala Lys Phe Ile Asn Lys Asp Glu Arg
            180   185   190

Ala Ala Met Ala Gly Asn Gln Asp Ser Thr Asn Val Tyr Val Lys Asn
        195   200   205

Leu Ile Glu Thr Val Thr Asp Asp Cys Leu His Thr Leu Phe Ser Gln
    210   215   220

Tyr Gly Thr Val Ser Ser Val Val Val Met Arg Asp Gly Met Gly Arg
225   230   235   240

Ser Arg Gly Phe Gly Phe Val Asn Phe Cys Asn Pro Glu Asn Ala Lys
            245   250   255

Lys Ala Met Glu Ser Leu Cys Gly Leu Gln Leu Gly Ser Lys Lys Leu
        260   265   270

Phe Val Gly Lys Ala Leu Lys Lys Asp Glu Arg Arg Glu Met Leu Lys
        275   280   285

208

Gln Lys Phe Ser Asp Asn Phe Ile Ala Lys Pro Asn Met Arg Trp Ser
    290   295   300

Asn Leu Tyr Val Lys Asn Leu Ser Glu Ser Met Asn Glu Thr Arg Leu
305   310   315   320

Arg Glu Ile Phe Gly Cys Tyr Gly Gln Ile Val Ser Ala Lys Val Met
            325   330   335

Cys His Glu Asn Gly Arg Ser Lys Gly Phe Gly Phe Val Cys Phe Ser
            340   345   350

Asn Cys Glu Glu Ser Lys Gln Ala Lys Arg Tyr Leu Asn Gly Phe Leu
            355   360   365

Val Asp Gly Lys Pro Ile Val Val Arg Val Ala Glu Arg Lys Glu Asp
    370   375   380

Arg Ile Lys Arg Leu Gln Gln Tyr Phe Gln Ala Gln Pro Arg Gln Tyr
385   390   395   400

Thr Gln Ala Pro Ser Ala Pro Ser Pro Ala Gln Pro Val Leu Ser Tyr
            405   410   415

Val Ser Ser Ser Tyr Gly Cys Phe Gln Pro Phe Gln Val Gly Thr Ser
            420   425   430

Tyr Tyr Tyr Met Gly Asn Gln Val Pro Gln Met Ser Gly His Gln Asn
            435   440   445

Ile Thr Thr Tyr Val Pro Ala Gly Lys Val Pro Leu Lys Glu Arg Arg
    450   455   460

Ser Met His Leu Val Tyr Lys His Pro Ala Tyr Pro Val Ala Lys Arg
465   470   475   480

Gly Ala Lys Gln Thr Leu Val Phe Lys Gly Glu Val Asn Arg Asn Leu
            485   490   495

Glu Ala Ala Thr Cys Ser Lys Ala Thr Thr Ser Glu Glu Asn Arg Lys
            500   505   510

Glu Glu Arg Arg Leu Thr Leu Ser Gly Lys Leu Ser Pro Glu Val Lys
            515   520   525

WO 03/008440   PCT/EP02/07929

Val Glu Glu Ser Gly Lys Gln Leu Gln
    530   535

<210> 93

<211> 657

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(657)

<223> ET3172

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Met Ala Phe Asp Glu Asp Met Lys Met Ala Ser Phe Leu Arg Glu Glu
1   5   10   15

gaa gaa caa cac tat tct tta tca aga ctc tcc gtt tgt tcc aac tac   96
Glu Glu Gln His Tyr Ser Leu Ser Arg Leu Ser Val Cys Ser Asn Tyr
            20   25   30

gac ggc gat gaa gcc gac ggt gag tct tct gct tcc gac gag aaa cgt   144
Asp Gly Asp Glu Ala Asp Gly Glu Ser Ser Ala Ser Asp Glu Lys Arg
        35   40   45

gtt gtc cac ggc gga gga gag aaa tcc atg gag gag cta aat ttt tca   192
Val Val His Gly Gly Gly Glu Lys Ser Met Glu Glu Leu Asn Phe Ser
    50   55   60

gat tct gat aaa gaa tca acc ggt tgt caa tct ctc ccg gcg aca cct   240
Asp Ser Asp Lys Glu Ser Thr Gly Cys Gln Ser Leu Pro Ala Thr Pro
65   70   75   80

ccg aga cgg aga cgg cgg aga ggc ggt gga gga gga gga tat tta gcg   288
Pro Arg Arg Arg Arg Arg Arg Gly Gly Gly Gly Gly Gly Tyr Leu Ala
                85   90   95

gtg agt tct ccg gtt tcc ggc gat aaa gct tac gct agc gag aac gaa   336
Val Ser Ser Pro Val Ser Gly Asp Lys Ala Tyr Ala Ser Glu Asn Glu
                100   105   110

gta caa aag acg aat aac aat cag agg aga agg agg aga ttg aaa ccg   384
Val Gln Lys Thr Asn Asn Asn Gln Arg Arg Arg Arg Arg Leu Lys Pro
            115   120   125

gag tgt cca ccg tgg gtt gat agt atg cgg agg agc tac gtc gga gat   432
Glu Cys Pro Pro Trp Val Asp Ser Met Arg Arg Ser Tyr Val Gly Asp
        130   135   140

210

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gaa cag agt agt cac ggt ggt tac gga gga gga gtg gtg gtt gtt acg      480
Glu Gln Ser Ser His Gly Gly Tyr Gly Gly Gly Val Val Val Val Thr
145             150             155             160

agg cct ata gga gga gga agg cca ttg tgt atg gat tta gaa gaa gtc      528
Arg Pro Ile Gly Gly Gly Arg Pro Leu Cys Met Asp Leu Glu Glu Val
                165             170             175

aaa gct tgt aaa gat ttg ggg ttt gag ctt gaa ccg ggt cgg gtt tcg      576
Lys Ala Cys Lys Asp Leu Gly Phe Glu Leu Glu Pro Gly Arg Val Ser
            180             185             190

tat tcc ggg tca acg gtg gat act agt agt ggc ggc aat tct cct atc      624
Tyr Ser Gly Ser Thr Val Asp Thr Ser Ser Gly Gly Asn Ser Pro Ile
            195             200             205

tct tct aac cac cgt att tcg agt ccc ggt tag                          657
Ser Ser Asn His Arg Ile Ser Ser Pro Gly
        210             215
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<210> 94

<211> 218

<212> PRT

<213> Arabidopsis thaliana

<400> 94

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Met Ala Phe Asp Glu Asp Met Lys Met Ala Ser Phe Leu Arg Glu Glu
1               5               10              15


Glu Glu Gln His Tyr Ser Leu Ser Arg Leu Ser Val Cys Ser Asn Tyr
            20              25              30


Asp Gly Asp Glu Ala Asp Gly Glu Ser Ser Ala Ser Asp Glu Lys Arg
            35              40              45


Val Val His Gly Gly Gly Glu Lys Ser Met Glu Glu Leu Asn Phe Ser
        50              55              60


Asp Ser Asp Lys Glu Ser Thr Gly Cys Gln Ser Leu Pro Ala Thr Pro
65              70              75              80


Pro Arg Arg Arg Arg Arg Arg Gly Gly Gly Gly Gly Gly Tyr Leu Ala
                85              90              95


Val Ser Ser Pro Val Ser Gly Asp Lys Ala Tyr Ala Ser Glu Asn Glu
            100             105             110
```

```
Val Gln Lys Thr Asn Asn Asn Gln Arg Arg Arg Arg Arg Leu Lys Pro
        115                 120             125


Glu Cys Pro Pro Trp Val Asp Ser Met Arg Arg Ser Tyr Val Gly Asp
        130             135             140


Glu Gln Ser Ser His Gly Gly Tyr Gly Gly Gly Val Val Val Val Thr
145                 150             155                 160


Arg Pro Ile Gly Gly Gly Arg Pro Leu Cys Met Asp Leu Glu Glu Val
                165             170             175


Lys Ala Cys Lys Asp Leu Gly Phe Glu Leu Glu Pro Gly Arg Val Ser
                180             185             190


Tyr Ser Gly Ser Thr Val Asp Thr Ser Ser Gly Gly Asn Ser Pro Ile
            195             200             205


Ser Ser Asn His Arg Ile Ser Ser Pro Gly
        210             215
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<210>   95

<211>   2220

<212>   DNA

<213>   Arabidopsis thaliana



<220>

<221>   CDS

<222>   (1)..(2220)

<223>   ET3546



<400>   95
atg gaa gct atg ctt gtg gac tgt gta aac aac agt ctt cgt cat ttt      48
Met Glu Ala Met Leu Val Asp Cys Val Asn Asn Ser Leu Arg His Phe
1               5                   10                  15

gtc tac aaa aat gct att ttc atg tgc gag cgt ctc tgc gct gag ttt      96
Val Tyr Lys Asn Ala Ile Phe Met Cys Glu Arg Leu Cys Ala Glu Phe
            20                  25                  30

cct tct gag gtt aat ttg cag cta tta gcc acc agc tac ctg cag aat     144
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212

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Pro Ser Glu Val Asn Leu Gln Leu Leu Ala Thr Ser Tyr Leu Gln Asn
        35              40                      45

aat caa gct tac agt gca tat cat ctg cta aag gga aca caa atg gct     192
Asn Gln Ala Tyr Ser Ala Tyr His Leu Leu Lys Gly Thr Gln Met Ala
    50              55                      60

cag tcc cga tac ttg ttc gca tta tca tgc ttc cag atg gac ctt ctc     240
Gln Ser Arg Tyr Leu Phe Ala Leu Ser Cys Phe Gln Met Asp Leu Leu
65              70                      75              80

aat gaa gct gaa tct gca ctc tgc cct gtt aat gaa cct ggt gcg gag     288
Asn Glu Ala Glu Ser Ala Leu Cys Pro Val Asn Glu Pro Gly Ala Glu
                85                      90                  95

atc cca aat ggt gca gca ggc cat tac ctt ctt gga ctt att tac aag     336
Ile Pro Asn Gly Ala Ala Gly His Tyr Leu Leu Gly Leu Ile Tyr Lys
                100             105                 110

aag aat gct gct caa caa ttt aaa cag tcc ttg aca ata gac cct cta     384
Lys Asn Ala Ala Gln Gln Phe Lys Gln Ser Leu Thr Ile Asp Pro Leu
                115                 120                 125

ctt tgg gct gca tat gag gaa tta tgt ata tta ggt gct gct gag gaa     432
Leu Trp Ala Ala Tyr Glu Glu Leu Cys Ile Leu Gly Ala Ala Glu Glu
        130                 135                 140

gca act gca gtt ttt ggt gaa aca gct gct ctc tcc att caa aag cag     480
Ala Thr Ala Val Phe Gly Glu Thr Ala Ala Leu Ser Ile Gln Lys Gln
145                 150                 155                 160

tat atg caa caa ctg tca act tcc ctc ggc tta aac act tac aac gag     528
Tyr Met Gln Gln Leu Ser Thr Ser Leu Gly Leu Asn Thr Tyr Asn Glu
                165                 170                 175

gaa cgt aat tca act tct act aaa aac acg agt tct gaa gat tat agt     576
Glu Arg Asn Ser Thr Ser Thr Lys Asn Thr Ser Ser Glu Asp Tyr Ser
            180                 185                 190

cca agg cag tct aaa cac aca caa agc cat ggc ctt aaa gat atc tcc     624
Pro Arg Gln Ser Lys His Thr Gln Ser His Gly Leu Lys Asp Ile Ser
            195                 200                 205

gga aat ttc cat tct cat gga gtt aat gga ggt gtt tcg aac atg tca     672
Gly Asn Phe His Ser His Gly Val Asn Gly Gly Val Ser Asn Met Ser
    210                 215                 220

ttc tat aat acg cct tcg cca gtg gct gca cag cta tcc ggt ata gct     720
Phe Tyr Asn Thr Pro Ser Pro Val Ala Ala Gln Leu Ser Gly Ile Ala
225                 230                 235                 240

cca cca cca ctt ttc cgg aat ttt cag cca gct gtt gca aac cca aac     768
Pro Pro Pro Leu Phe Arg Asn Phe Gln Pro Ala Val Ala Asn Pro Asn
                245                 250                 255

tcc ctt att act gac agt tct cca aag tcc act gtt aac tct act ctt     816
Ser Leu Ile Thr Asp Ser Ser Pro Lys Ser Thr Val Asn Ser Thr Leu
                260                 265                 270

caa gca cct aga aga aag ttt gta gat gaa gga aag tta cgt aag att     864
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213

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        Gln Ala Pro Arg Arg Lys Phe Val Asp Glu Gly Lys Leu Arg Lys Ile
                275                     280                 285

tct ggc aga cta ttt tct gat tct ggt cca cga cgg agt tca aga ctg          912
Ser Gly Arg Leu Phe Ser Asp Ser Gly Pro Arg Arg Ser Ser Arg Leu
        290                     295                 300

tct gct gat tca ggg gca aac att aat tca agt gtt gca aca gta agc          960
Ser Ala Asp Ser Gly Ala Asn Ile Asn Ser Ser Val Ala Thr Val Ser
305                     310                 315                 320

gga aat gtg aac aac gct tcc aag tat ttg gga ggt tct aaa ttg agt         1008
Gly Asn Val Asn Asn Ala Ser Lys Tyr Leu Gly Gly Ser Lys Leu Ser
                    325                 330                 335

tct ttg gca ctt cgt tct gta aca ctt cgg aag gga cac tcc tgg gca        1056
Ser Leu Ala Leu Arg Ser Val Thr Leu Arg Lys Gly His Ser Trp Ala
                340                     345                 350

aat gaa aac atg gat gaa ggg gtc cgt ggg gaa cct ttt gat gat tca        1104
Asn Glu Asn Met Asp Glu Gly Val Arg Gly Glu Pro Phe Asp Asp Ser
            355                     360                 365

agg cct aat act gcc tca acg act ggt tct atg gct tcc aat gat caa        1152
Arg Pro Asn Thr Ala Ser Thr Thr Gly Ser Met Ala Ser Asn Asp Gln
        370                     375                 380

gaa gac gaa aca atg tcg att ggt ggc ata gca atg agt tct caa aca        1200
Glu Asp Glu Thr Met Ser Ile Gly Gly Ile Ala Met Ser Ser Gln Thr
385                     390                 395                 400

atc aca att ggt gtt tcg gaa att tta aac ctc ctt agg aca ctc gga        1248
Ile Thr Ile Gly Val Ser Glu Ile Leu Asn Leu Leu Arg Thr Leu Gly
                    405                 410                 415

gaa ggg tgt aga ctt tca tac atg tac agg tgt cag gag gca ctg gat        1296
Glu Gly Cys Arg Leu Ser Tyr Met Tyr Arg Cys Gln Glu Ala Leu Asp
                420                     425                 430

acg tat atg aaa ctt cca cat aag cat tat aat aca gga tgg gtt ctt        1344
Thr Tyr Met Lys Leu Pro His Lys His Tyr Asn Thr Gly Trp Val Leu
            435                     440                 445

tcc cag gtc ggg aaa gca tac ttt gaa cta att gac tat tta gag gct        1392
Ser Gln Val Gly Lys Ala Tyr Phe Glu Leu Ile Asp Tyr Leu Glu Ala
        450                     455                 460

gaa aag gca ttc cgt ctt gcc cgt ctg gct tct cct tat tgc tta gaa        1440
Glu Lys Ala Phe Arg Leu Ala Arg Leu Ala Ser Pro Tyr Cys Leu Glu
465                     470                 475                 480

gga atg gat ata tac tct acg gtc ctc tat cat ttg aag gaa gac atg        1488
Gly Met Asp Ile Tyr Ser Thr Val Leu Tyr His Leu Lys Glu Asp Met
                    485                 490                 495

aag ctg agt tac ttg gct cag gaa cta ata tca acc gat cgc tta gct        1536
Lys Leu Ser Tyr Leu Ala Gln Glu Leu Ile Ser Thr Asp Arg Leu Ala
                500                     505                 510

cct caa tct tgg tgt gct atg gga aat tgc tat agc ttg caa aag gac        1584
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214

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Pro Gln Ser Trp Cys Ala Met Gly Asn Cys Tyr Ser Leu Gln Lys Asp
        515                 520                 525

cat gag acc gca ctg aag aat ttc cta cga gct gtt caa ctg aat cca    1632
His Glu Thr Ala Leu Lys Asn Phe Leu Arg Ala Val Gln Leu Asn Pro
        530                 535                 540

aga ttt gca tat gca cat acc tta tgt ggc cac gaa tac aca act ctt    1680
Arg Phe Ala Tyr Ala His Thr Leu Cys Gly His Glu Tyr Thr Thr Leu
545                 550                 555                 560

gag gat ttt gag aac gga atg aaa agt tac caa aac gca ctt cgt gta    1728
Glu Asp Phe Glu Asn Gly Met Lys Ser Tyr Gln Asn Ala Leu Arg Val
                565                 570                 575

gat aca aga cac tac aac gca tgg tac ggg ctt gga atg ata tat cta    1776
Asp Thr Arg His Tyr Asn Ala Trp Tyr Gly Leu Gly Met Ile Tyr Leu
                580                 585                 590

cgc caa gag aag tta gag ttc tca gag cat cac ttc aga atg gct ttc    1824
Arg Gln Glu Lys Leu Glu Phe Ser Glu His His Phe Arg Met Ala Phe
                595                 600                 605

cta ata aac ccg agt tcc tct gtt ata atg tct tat tta ggg aca tct    1872
Leu Ile Asn Pro Ser Ser Ser Val Ile Met Ser Tyr Leu Gly Thr Ser
        610                 615                 620

ttg cat gcc ttg aag aga agt gag gaa gca cta gag ata atg gag caa    1920
Leu His Ala Leu Lys Arg Ser Glu Glu Ala Leu Glu Ile Met Glu Gln
625                 630                 635                 640

gcc ata gta gca gat aga aaa aac cct ctt cca atg tac cag aaa gct    1968
Ala Ile Val Ala Asp Arg Lys Asn Pro Leu Pro Met Tyr Gln Lys Ala
                645                 650                 655

aac ata ctt gtc tgc tta gaa aga tta gat gaa gct cta gaa gtt ctt    2016
Asn Ile Leu Val Cys Leu Glu Arg Leu Asp Glu Ala Leu Glu Val Leu
                660                 665                 670

gag gag ctc aaa gag tat gcg cct tca gag agc agc gtt tac gct tta    2064
Glu Glu Leu Lys Glu Tyr Ala Pro Ser Glu Ser Ser Val Tyr Ala Leu
        675                 680                 685

atg ggc agg atc tat aag cgg cga aac atg cac gat aaa gcc atg ctt    2112
Met Gly Arg Ile Tyr Lys Arg Arg Asn Met His Asp Lys Ala Met Leu
        690                 695                 700

cat ttc ggt cta gct tta gat atg aaa ccg cct gca act gac gtt gct    2160
His Phe Gly Leu Ala Leu Asp Met Lys Pro Pro Ala Thr Asp Val Ala
705                 710                 715                 720

gca ata aag gct gca atg gag aaa ttg cat gtt cca gat gag atc gat    2208
Ala Ile Lys Ala Ala Met Glu Lys Leu His Val Pro Asp Glu Ile Asp
                725                 730                 735

gag agc ccg tga                                                    2220
Glu Ser Pro
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<210> 96

<211> 739

<212> PRT

<213> Arabidopsis thaliana

<400> 96

Met Glu Ala Met Leu Val Asp Cys Val Asn Asn Ser Leu Arg His Phe
1   5   10   15

Val Tyr Lys Asn Ala Ile Phe Met Cys Glu Arg Leu Cys Ala Glu Phe
                20   25   30

Pro Ser Glu Val Asn Leu Gln Leu Leu Ala Thr Ser Tyr Leu Gln Asn
            35   40   45

Asn Gln Ala Tyr Ser Ala Tyr His Leu Leu Lys Gly Thr Gln Met Ala
        50   55   60

Gln Ser Arg Tyr Leu Phe Ala Leu Ser Cys Phe Gln Met Asp Leu Leu
65   70   75   80

Asn Glu Ala Glu Ser Ala Leu Cys Pro Val Asn Glu Pro Gly Ala Glu
                85   90   95

Ile Pro Asn Gly Ala Ala Gly His Tyr Leu Leu Gly Leu Ile Tyr Lys
            100   105   110

Lys Asn Ala Ala Gln Gln Phe Lys Gln Ser Leu Thr Ile Asp Pro Leu
        115   120   125

Leu Trp Ala Ala Tyr Glu Glu Leu Cys Ile Leu Gly Ala Ala Glu Glu
    130   135   140

Ala Thr Ala Val Phe Gly Glu Thr Ala Ala Leu Ser Ile Gln Lys Gln
145   150   155   160

Tyr Met Gln Gln Leu Ser Thr Ser Leu Gly Leu Asn Thr Tyr Asn Glu
                165   170   175

Glu Arg Asn Ser Thr Ser Thr Lys Asn Thr Ser Ser Glu Asp Tyr Ser
            180   185   190

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Pro Arg Gln Ser Lys His Thr Gln Ser His Gly Leu Lys Asp Ile Ser
        195             200         205


Gly Asn Phe His Ser His Gly Val Asn Gly Gly Val Ser Asn Met Ser
    210             215             220


Phe Tyr Asn Thr Pro Ser Pro Val Ala Ala Gln Leu Ser Gly Ile Ala
225             230             235             240


Pro Pro Pro Leu Phe Arg Asn Phe Gln Pro Ala Val Ala Asn Pro Asn
            245             250             255


Ser Leu Ile Thr Asp Ser Ser Pro Lys Ser Thr Val Asn Ser Thr Leu
            260             265             270


Gln Ala Pro Arg Arg Lys Phe Val Asp Glu Gly Lys Leu Arg Lys Ile
        275             280             285


Ser Gly Arg Leu Phe Ser Asp Ser Gly Pro Arg Arg Ser Ser Arg Leu
    290             295             300


Ser Ala Asp Ser Gly Ala Asn Ile Asn Ser Ser Val Ala Thr Val Ser
305             310             315             320


Gly Asn Val Asn Asn Ala Ser Lys Tyr Leu Gly Gly Ser Lys Leu Ser
            325             330             335


Ser Leu Ala Leu Arg Ser Val Thr Leu Arg Lys Gly His Ser Trp Ala
            340             345             350


Asn Glu Asn Met Asp Glu Gly Val Arg Gly Glu Pro Phe Asp Asp Ser
        355             360             365


Arg Pro Asn Thr Ala Ser Thr Thr Gly Ser Met Ala Ser Asn Asp Gln
    370             375             380


Glu Asp Glu Thr Met Ser Ile Gly Gly Ile Ala Met Ser Ser Gln Thr
385             390             395             400


Ile Thr Ile Gly Val Ser Glu Ile Leu Asn Leu Leu Arg Thr Leu Gly
            405             410             415


Glu Gly Cys Arg Leu Ser Tyr Met Tyr Arg Cys Gln Glu Ala Leu Asp
            420             425             430
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217

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Thr Tyr Met Lys Leu Pro His Lys His Tyr Asn Thr Gly Trp Val Leu
        435                 440                 445


Ser Gln Val Gly Lys Ala Tyr Phe Glu Leu Ile Asp Tyr Leu Glu Ala
        450                 455                 460


Glu Lys Ala Phe Arg Leu Ala Arg Leu Ala Ser Pro Tyr Cys Leu Glu
465                 470                 475                 480


Gly Met Asp Ile Tyr Ser Thr Val Leu Tyr His Leu Lys Glu Asp Met
                485                 490                 495


Lys Leu Ser Tyr Leu Ala Gln Glu Leu Ile Ser Thr Asp Arg Leu Ala
            500                 505                 510


Pro Gln Ser Trp Cys Ala Met Gly Asn Cys Tyr Ser Leu Gln Lys Asp
            515                 520                 525


His Glu Thr Ala Leu Lys Asn Phe Leu Arg Ala Val Gln Leu Asn Pro
    530                 535                 540


Arg Phe Ala Tyr Ala His Thr Leu Cys Gly His Glu Tyr Thr Thr Leu
545                 550                 555                 560


Glu Asp Phe Glu Asn Gly Met Lys Ser Tyr Gln Asn Ala Leu Arg Val
                565                 570                 575


Asp Thr Arg His Tyr Asn Ala Trp Tyr Gly Leu Gly Met Ile Tyr Leu
            580                 585                 590


Arg Gln Glu Lys Leu Glu Phe Ser Glu His His Phe Arg Met Ala Phe
        595                 600                 605


Leu Ile Asn Pro Ser Ser Ser Val Ile Met Ser Tyr Leu Gly Thr Ser
    610                 615                 620


Leu His Ala Leu Lys Arg Ser Glu Glu Ala Leu Glu Ile Met Glu Gln
625                 630                 635                 640


Ala Ile Val Ala Asp Arg Lys Asn Pro Leu Pro Met Tyr Gln Lys Ala
                645                 650                 655


Asn Ile Leu Val Cys Leu Glu Arg Leu Asp Glu Ala Leu Glu Val Leu
            660                 665                 670
```

218

Glu Glu Leu Lys Glu Tyr Ala Pro Ser Glu Ser Ser Val Tyr Ala Leu
        675   680   .685

Met Gly Arg Ile Tyr Lys Arg Arg Asn Met His Asp Lys Ala Met Leu
        690   695   700

His Phe Gly Leu Ala Leu Asp Met Lys Pro Pro Ala Thr Asp Val Ala
705   710   715   720

Ala Ile Lys Ala Ala Met Glu Lys Leu His Val Pro Asp Glu Ile Asp
            725   730   735

Glu Ser Pro

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<213>   Arabidopsis thaliana

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<223>   n = a, t, c, or g


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<223>  n = a, t, c, or g


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<211>  16

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<223>  n = a, t, c, or g


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221

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<223>   n = a, t, c, or g
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222

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ntcgastwts gwgtt                                                    15


<210>  107

<211>  16

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  CA55

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<222>  (1)..(16)

<223>  n = a, t, c, or g


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wgtgnagwan canaga                                                   16


<210>  108

<211>  30

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  5A

<400>  108
actagctcta ccgtttccgt ttccgtttac                                   30


<210>  109

<211>  30

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<220>

<223> 5B

<400> 109
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<210> 110

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<223> 5C

<400> 110
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<223> 3A

<400> 111
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<223> 3C

<400> 113
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<400> 114
attaggcacc ccaggcttta cactttatg   29

<210> 115

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<223> CA67

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<210> 30

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<223> CA68

<400> 116
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<210> 117

<211> 34

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<223> JM33

<400> 117
tagcatctga atttcataac caatctcgat acac   34

<210> 118

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> JM34

<400> 118
gcttcctatt atatcttccc aaattaccaa taca   34

<210> 119

<211> 34

<212> DNA

<213> Artificial Sequence

226

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<223>  JM35

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<212>  DNA

<213>  Artificial Sequence



<220>

<223>  QRB1

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<210>  121

<211>  32

<212>  DNA

<213>  Artificial Sequence



<220>

<223>  QRB2

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<211>  30

<212>  DNA

<213>  Artificial Sequence



<220>

<223>  QRB3
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<210>  123

<211>  35

<212>  DNA

<213>  Artificial Sequence



<220>

<223>  SKI1

<400>  123
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<210>  124

<211>  31

<212>  DNA

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<220>

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<400>  124
atattgacca tcatactcat tgctgatcca t                           31


<210>  125

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<212>  DNA

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<220>

<223>  SKI3

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tgatccatgt agatttcccg gacatgaa                               28
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228

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